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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:09:23 ; Search time 45 Seconds
(without alignments)
821.851 Million cell updates/sec

Title: US-09-909-005-1

Perfect score: 1170

Sequence: 1 MLKPSVTSAPTADMTLVV.....LLIQQQQQQQQQQQQNHMS 233

Scoring table: BUCSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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24: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1170	100.0	233	20 AAY29978	Human cell junctio
2	1170	100.0	233	22 AAU07127	Human cell junctio
3	1170	100.0	233	23 AAU93326	Human cell junctio
4	814	69.6	197	22 AAM78892	Human protein sequ
5	814	69.6	197	22 AAB93600	Human protein sequ
6	814	69.6	198	22 AAM79876	Human protein sequ
7	807	69.0	207	22 AAE03655	Human extracellular
8	807	69.0	207	22 AAU93629	Human PRO protein,
9	754	64.4	195	22 ABB63428	Drosophila melanog

10	669	57.2	167	22	AAU17388	Novel signal trans
11	579	49.5	163	22	AAU17399	Novel signal trans
12	575	49.1	150	21	AAB43364	Human ORFX ORF3128
13	472	40.3	97	22	AAB55836	PDZ encoded domain
14	472	40.3	97	22	AAB57627	Tax interaction pr
15	472	40.3	97	22	AAB58037	Tax interaction pr
16	472	40.3	97	23	ABJ05302	PDZ domain protein
17	467	39.9	91	23	ABP63172	TXA-IP 33 PDZ doma
18	208.5	17.8	960	22	ABP63172	Drosophila melanog
19	203.5	17.4	817	19	AAW48101	Human discs large
20	203.5	17.4	817	20	AAJ30137	Amino acid sequenc
21	203.5	17.4	849	19	AAW48102	Human discs large
22	197.5	16.9	882	18	AAW34662	Partial PSD-93 pro
23	196.5	16.8	724	23	ABB04798	LDL receptor bindi
24	196.5	16.8	767	23	ABP65167	Hypoxia-regulated
25	196.5	16.8	767	23	AAU84269	Human endometrial
26	196.5	16.8	767	23	AAU84328	Protein DLG4 diffe
27	194.5	16.6	767	21	AAJ22138	Human post-synapti
28	190.5	16.3	85	23	AAU87939	Human PDZ domain #
29	190	16.2	1881	20	AAJ24025	Amino acid sequenc
30	181.5	15.5	344	22	AAB55834	PDZ encoded domain
31	181.5	15.5	344	22	AAB57623	Human post-synapti
32	181.5	15.5	344	22	AAB58035	Human post-synapti
33	181.5	15.5	344	23	ABJ05300	PDZ domain protein
34	180.5	15.4	338	23	ABP63160	Human PSD95 PDZ do
35	180.5	15.4	442	23	ABP63536	Human PSD95 PDZ do
36	180.5	15.4	724	23	ABB04807	LDL receptor bindi
37	180.5	15.4	2466	16	AAJ71498	Human protein tyro
38	180.5	15.4	2466	19	AAJ75999	Intracellular prot
39	180.5	15.4	2466	21	AAJ90272	Human PrPL1 phosph
40	176.5	15.1	763	20	AAJ04731	PDZ domain-contains
41	176.5	15.1	1005	20	AAJ04731	Mature protein con
42	176.5	15.1	1373	20	AAJ04730	Protein containing
43	176.5	15.1	2000	20	AAJ04732	Protein containing
44	176.5	15.1	2070	20	AAJ04733	Protein containing
45	174.5	14.9	304	22	AAM93296	Human polypeptide,

ALIGNMENTS

RESULT 1
AAY29978
ID AAY29978 standard; Protein; 233 AA.
XX
AC AAY29978;
XX
DT 23-NOV-1999 (first entry)
XX
DE Human cell junction PDZ protein CJPDPZ.
XX
DE Human; cell junction PDZ protein; PDZ domain; CJPDPZ; diagnosis;
KW cancer; neurological disorder; developmental disorder;
KW William's syndrome.
XX
OS Homo sapiens.
XX
PN US5958731-A.
XX
PD 28-SEP-1999.
XX
PF 11-SEP-1998; 98US-0151611.
XX
PR 11-SEP-1998; 98US-0151611.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Patterson C, Au-Young J;
XX
DR WPI: 1999-561035/47.
DR N-FSDB; AA221259.
XX
PT Nucleic acids encoding cellular junction PDZ protein domains useful in

PT the prevention, diagnosis and treatment of disorders associated with
 PT defective cell signalling such as cancers and neurological and
 PT developmental disorders -
 PS Claim 1; Column 39-40; 27pp; English.
 XX
 CC The present sequence represents human cell junction PDZ protein (CJPDZ).
 CC CJPDZ polynucleotides and proteins may be used in the diagnosis,
 CC prevention and treatment of disorders associated with defective cell
 CC signalling. They may be used to treat cancers, neurological disorders
 CC and developmental disorders such as William's syndrome. CJPDZ or vectors
 CC containing CJPDZ may be administered to treat any of the above diseases
 CC by rectifying mutations or deletions in a patient's genome that affect
 CC cell signalling by expressing inactive proteins or to supplement the
 CC patients own production of CJPDZ protein domains. Antisense nucleic acid
 CC molecules may be administered to down regulate CJPDZ protein domain
 CC expression by binding with the cells own CJPDZ genes and preventing
 CC their expression. CJPDZ polynucleotides may also be used as DNA probes
 CC in diagnostic assays to detect and quantitate the presence of similar
 CC nucleic acid sequences in samples, and hence which patients may be in
 CC need of restorative therapy. They may also be used to study the
 CC expression and function of CJPDZ protein domains and their role in
 CC cellular signalling. The CJPDZ protein domains may be used as antigens
 CC in the production of antibodies and in assays to identify modulators
 CC of CJPDZ expression and activity.
 XX SQ Sequence 233 AA;

Query Match 100.0%; Score 1170; DB 20; Length 233;
 Best Local Similarity 100.0%; Pred. No. 3.3e-108;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLKPSVTSAPTADMATLVVQPLTDRDVARAIELLEKLOESGVPVHKLSLKKVQSE 60
 Db 1 MLKPSVTSAPTADMATLVVQPLTDRDVARAIELLEKLOESGVPVHKLSLKKVQSE 60
 Qy 61 FCTAIRVYQYMHETITVNGCPEFRARATATVAFAAASGSHSPRVVLPKTDGLGF 120
 Db 61 FCTAIRVYQYMHETITVNGCPEFRARATATVAFAAASGSHSPRVVLPKTDGLGF 120
 Qy 121 NVMGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSVEGHEHKAVELLKAAD 180
 Db 121 NVMGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSVEGHEHKAVELLKAAD 180
 Qy 181 SVKLIVRYTPKLVLEMEARFEKLTARRRQOQLLIQOQQOQQOQQOQQOQHMS 233
 Db 181 SVKLIVRYTPKLVLEMEARFEKLTARRRQOQLLIQOQQOQQOQQOQQOQHMS 233

RESULT 2
 AAU07127
 ID AAU07127 standard; Protein; 233 AA.
 XX AC AAU07127;
 XX AC
 XX 24-OCT-2001 (first entry)
 XX DE Human cell junction PDZ protein, CJPDZ.
 XX KW Human; cell junction PDZ protein; CJPDZ; antigen; antibody; cytostatic;
 KW anti-leukaemic; neuroprotective; antiepileptic; anti-Alzheimer's disease;
 KW neurotropic; anti-convulsant; cancer; leukaemia; myeloma; sarcoma;
 KW neurological disorder; epilepsy; Alzheimer's disease;
 KW Huntington's chorea.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX Domain 107..189
 XX FT /label= PDZ_domain
 XX PN US6265547-B1.
 XX KW

PD 24-JUL-2001.
 XX 06-AUG-1999; 99US-0370102.
 XX 11-SEP-1998; 98US-0151611.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Yue H, Au-young J, Patterson C;
 PI WPI; 2001-463943/50.
 XX N-PSDB; AAS11583.
 DR Cellular junction PDZ proteins useful in the prevention, diagnosis and
 DR treatment of disorders associated with defective cell signalling such as
 PT cancers, neurological disorders and developmental disorders such as
 PT William's syndrome -
 PT Claim 1; Fig 1; 28pp; English.

The invention relates to a purified human cell junction PDZ (CJPDZ) polypeptide. The polypeptide may be used as an antigen in the production of antibodies against CJPDZ and in assays to identify molecules which bind CJPDZ including modulators of CJPDZ expression and activity. The anti-CJPDZ antibodies, agonists and antagonists may be used to control/regulate expression and activity of CJPDZ. The anti-CJPDZ antibodies may also be used as diagnostic agents for detecting the presence of CJPDZ polypeptides in samples (e.g. by enzyme linked immunosorbent assay, ELISA). Disorders of cell signalling and CJPDZ expression and activity that may be prevented, diagnosed and/or treated by the above methods include, for example cancers (e.g. leukaemia, myeloma, sarcoma or lung, liver, colon or spleen cancer), neurological disorders (e.g. epilepsy, Alzheimer's disease and/or Huntington's chorea). A full list of disorders that may be treated is given in the CC specification. The present sequence represents human CJPDZ.

XX SQ Sequence 233 AA;

Query Match 100.0%; Score 1170; DB 22; Length 233;
 Best Local Similarity 100.0%; Pred. No. 3.3e-108;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLKPSVTSAPTADMATLVVQPLTDRDVARAIELLEKLOESGVPVHKLSLKKVQSE 60
 Db 1 MLKPSVTSAPTADMATLVVQPLTDRDVARAIELLEKLOESGVPVHKLSLKKVQSE 60
 Qy 61 FCTAIRVYQYMHETITVNGCPEFRARATATVAFAAASGSHSPRVVLPKTDGLGF 120
 Db 61 FCTAIRVYQYMHETITVNGCPEFRARATATVAFAAASGSHSPRVVLPKTDGLGF 120
 Qy 121 NVMGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSVEGHEHKAVELLKAAD 180
 Db 121 NVMGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSVEGHEHKAVELLKAAD 180
 Qy 181 SVKLIVRYTPKLVLEMEARFEKLTARRRQOQLLIQOQQOQQOQQOQHMS 233
 Db 181 SVKLIVRYTPKLVLEMEARFEKLTARRRQOQLLIQOQQOQQOQQOQHMS 233

RESULT 3

AAU99326
 ID AAU99326 standard; Protein; 233 AA.
 XX AC AAU99326;
 XX AC

XX 07-OCT-2002 (first entry)

XX Human cell junction PDZ (CJPDZ) protein.

XX Human; cytostatic; neurotropic; neuroprotective; endocrine;
 KW cell junction PDZ; CJPDZ; membrane-associated signalling protein;
 KW signal transduction; postsynaptic density protein 95; PSD-95;
 KW Drosophila lethal (1) discs large-1; Dig; zonula occludens-1; ZO-1;

Db 6 EPVRLERDICRAIELLEKQSGEVPKQALQALQRLQSEFCNAYREVYEHVETVDISS 65
QY 81 CPEFRARATATVAATFAASGSHSPRVVLPKTDGEGFNVMGKEQNSPIYISRIIPG 140
Db 66 SPEVRANATATVAATFAASGSHSPRVVLPKTEEGGFGNMGKEQNSPIYISRIIPG 125
QY 141 GVAERHGLKRGDQLLSVNGSVGEHEHEKAVELLKAAKDSVKLVVRYTPKVLMEARF 200
Db 126 GIADRHGGLKRGDQLLSVNGSVGEHEHEKAVELLKAAQGVKLVVRYTPKVLMEARF 185
QY 201 EKLRTARRRQ 211
Db 186 EKMSAKRRQ 196

RESULT 5
AAB93600
ID AAB93600 standard; Protein; 197 AA.
AC AAB93600;
XX 26-JUN-2001 (first entry)
DE Human protein sequence SEQ ID NO:13038.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 13038; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 197 AA;
Query Match 69.6%; Score 814; DB 22; Length 197;
Best Local Similarity 80.6%; Pred. No. 8e-73;
Matches 154; Conservative 24; Mismatches 13; Indels 0; Gaps 0;
QY 21 QPLTLDRDVARAIELLEKIQSGEVPVHKLQSLKVLQSEFCTATREYVOYMHETVNG 80
Db 6 EPVRLERDICRAIELLEKQSGEVPKQALQALQRLQSEFCNAYREVYEHVETVDISS 65
QY 81 CPEFRARATATVAATFAASGSHSPRVVLPKTDGEGFNVMGKEQNSPIYISRIIPG 140
Db 66 SPEVRANATATVAATFAASGSHSPRVVLPKTEEGGFGNMGKEQNSPIYISRIIPG 125
QY 141 GVAERHGLKRGDQLLSVNGSVGEHEHEKAVELLKAAKDSVKLVVRYTPKVLMEARF 200
Db 126 GIADRHGGLKRGDQLLSVNGSVGEHEHEKAVELLKAAQGVKLVVRYTPKVLMEARF 185
QY 201 EKLRTARRRQ 211
Db 186 EKMSAKRRQ 196

RESULT 6
AAM79876
ID AAM79876 standard; Protein; 198 AA.
XX
AC AAM79876;
XX
DT 06-NOV-2001 (first entry)
DE Human protein SEQ ID NO 3522.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-ESDB; AAK53009.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 370; 6221pp; English.

PR	26-JUL-2000;	2000US-02209660;
PR	14-AUG-2000;	2000US-02245118;
PR	14-AUG-2000;	2000US-02245119;
PR	14-AUG-2000;	2000US-02245119;
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PR	14-SEP-2000;	2000US-02324401;
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PR	21-SEP-2000;	2000US-02342774;
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PR	02-OCT-2000;	2000US-02370338;
PR	02-OCT-2000;	2000US-02370339;
PR	02-OCT-2000;	2000US-02370440;
PR	13-OCT-2000;	2000US-02399335;
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PR	20-OCT-2000;	2000US-02412221;
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PR	20-OCT-2000;	2000US-02418009;
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PR	08-NOV-2000;	2000US-02464474;
PR	08-NOV-2000;	2000US-02464475;

PR 26-JUL-2000; 2000US-0220963.
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 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
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 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236570.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244517.
 PR 08-NOV-2000; 2000US-0246474.

PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0254097.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-465460/50.
 DR N-PSDB; AAS27316.

Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders -
 XX
 PS Claim 1; SEQ ID No 964; 880pp; English.

CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
 CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal

disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. Addison's disease), reproductive system disorders, gastrointestinal disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction pathway protein, amino acid sequences of the invention.

Query Match 49.5%; Score 579; DB 22; Length 163;
Best Local Similarity 84.1%; Pred. No. 1.6e-49;
Matches 111; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 82 PFRARAKATVAFAASEGSHPRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGG 141
DB 23 PHQLSLSQATVAFTAEGHAHPRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGG 82
QY 142 VAERHGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVVRYTPKVLMEARFE 201
DB 83 VADRHGGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVVRYTPKVLMEARFE 142
QY 202 KLRTARRRQQQ 213
DB 143 KMRSARRRQQHQ 154

RESULT 12

AA043364
ID AAB43364 standard; Protein; 150 AA.

AC AAB43364;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF3128 polypeptide sequence SEQ ID NO:6256.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotrophic; antidiabetic; hypotensive; dermatological; immunosuppressive; antirheumatic; antithyroid; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US08621.

PR 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 30-MAR-2000; 2000US-0540763.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

XX WPI; 2000-602362/57.

DR N-PSDB; AAC7573.

XX

Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Claim 11; Page 5443; 5507pp; English.

AA074446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.

Sequence 150 AA;

Query Match 49.1%; Score 575; DB 21; Length 150;

Best Local Similarity 90.2%; Pred. No. 3.6e-49;

Matches 111; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 91 KATVAFAAASEGSHPRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGGVAERHGLK 150
DB 19 KATVAFTAEGHAHPRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGGVADRHGLK 78

QY 151 RGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVVRYTPKVLMEARFEKLRTARRRQ 210
DB 79 RGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVVRYTPKVLMEARFEKLRTARRRQ 138

QY 211 QQQ 213

DB 139 QHQ 141

RESULT 13

AA055836

ID AAB55836 standard; Peptide; 97 AA.

AC AAB55836;

DT 07-MAR-2001 (first entry)

PDZ encoded domain #6.

Human; open reading frame; PDZ; antiinflammatory; inflammation; allergy; asthma; multiple sclerosis; cancer; infection.

OS Synthetic.

PN WO200069896-A2.

PD 23-NOV-2000.

PF 12-MAY-2000; 2000WO-US13161.

PR 14-MAY-1999; 99US-0134114.

PR 14-MAY-1999; 99US-0134117.

PR 14-MAY-1999; 99US-0134118.

PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX (ARBO-) ARBOR VITA CORP.
 XX Lu PS;

PI WPI; 2001-080245/09.
 XX Modulating a biological function of an endothelial cell or
 XX hematopoietic cell, useful for treating autoimmune diseases and
 XX infectious diseases, by administering an antagonist that inhibits
 XX binding between a PDZ protein and a PL protein -

XX Disclosure; Page 28-43; 141pp; English.

XX The present invention relates to a new method for modulating a
 CC biological function of an endothelial cell or hematopoietic cell. The
 CC method involves introducing into a cell, an antagonist that inhibits
 CC binding between a PDZ protein and a PL protein. The inhibitor is used
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
 CC disease. It may also be used to prevent transplantation rejection of
 CC a solid organ transplant. The method may also be used in the treatment
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
 CC graft rejection, transplantation rejection), atherosclerosis, cancers,
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.
 XX Sequence 97 AA;

Query Match 40.3%; Score 472; DB 22; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.6e-39;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 HSHPRVVELPKTDEGLGFNVMGKEQNSPIYISRIIPGGVAERHGGIKRGDQLLSVNGVS 162
 Db 1 HSHPRVVELPKTDEGLGFNVMGKEQNSPIYISRIIPGGVAERHGGIKRGDQLLSVNGVS 60
 QY 163 VEGEHKAVELLKAAKDSVKLVRYTPKYLE 194
 Db 61 VEGEHKAVELLKAAKDSVKLVRYTPKYLE 92

RESULT 14
 AAB57627
 ID AAB57627 standard; Protein; 97 AA.

XX AAB57627;
 XX 12-MAR-2001 (first entry)

XX Tax interaction protein 33 PDZ domain.

XX Endothelial cell; hematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; synapse formation;
 KW transmembrane neurotransmitter receptor; autoimmune disease;
 KW transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.
 XX WO200069897-A2.

XX 23-NOV-2000.

XX

PF 12-MAY-2000; 2000WO-US13166.
 XX 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX (ARBO-) ARBOR VITA CORP.
 XX Lu PS;

PI WPI; 2001-025003/03.

XX New inhibitors of binding of a PDZ protein and PL protein for
 XX inhibiting T cell-mediated response by hematopoietic cells, or for
 XX treating diseases characterized by inflammatory and humoral immune
 XX responses, e.g. inflammation, cancer -
 XX Disclosure; Page 30; 139pp; English.

XX The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or hematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a PDZ domain. PDZ domains
 CC of proteins are named after three prototypical proteins: PSD95,
 CC Drosophila large disc protein and Zonula Occludin 1 protein. PDZ domain
 CC proteins are involved in synapse formation by organising transmembrane
 CC neurotransmitter receptors through intracellular interactions. The
 CC inhibitors identified by the present invention can be used to treat a
 CC disease mediated by hematopoietic cells, e.g. autoimmune disease,
 CC inflammation, allergy (e.g. drug allergies), inflammatory bowel diseases,
 CC ulcerative colitis, ileitis, psoriasis, respiratory allergic diseases
 CC (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto
 CC thyroiditis, osteoarthritis), atherosclerosis, cancers, infectious
 CC diseases (e.g. viral infection), ischaemia, vasculitis and Crohn's
 CC disease. The inhibitors can also be used to prevent transplantation
 CC rejection of a solid organ transplant.

XX Sequence 97 AA;

Query Match 40.3%; Score 472; DB 22; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.6e-39;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 HSHPRVVELPKTDEGLGFNVMGKEQNSPIYISRIIPGGVAERHGGIKRGDQLLSVNGVS 162
 Db 1 HSHPRVVELPKTDEGLGFNVMGKEQNSPIYISRIIPGGVAERHGGIKRGDQLLSVNGVS 60
 QY 163 VEGEHKAVELLKAAKDSVKLVRYTPKYLE 194
 Db 61 VEGEHKAVELLKAAKDSVKLVRYTPKYLE 92

RESULT 15
 AAB58037
 ID AAB58037 standard; Protein; 97 AA.

XX AAB58037;

XX 12-MAR-2001 (first entry)

XX Tax interaction protein 33 PDZ domain.

XX Endothelial cell; hematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; synapse formation;

Search completed: September 23, 2003, 15:13:53
Job time : 47 secs

KW transmembrane neurotransmitter receptor; autoimmune disease;
KW transplantation rejection; inflammation; allergy;
KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.

OS
XX
XX WO200069898-A2.

PN
XX
XX 23-NOV-2000.

PD
XX
XX 12-MAY-2000; 2000WO-US13205.

XX
XX 14-MAY-1999; 99US-0134114.

PR
XX 14-MAY-1999; 99US-0134117.

PR
XX 14-MAY-1999; 99US-0134118.

PR
XX 21-OCT-1999; 99US-0160860.

PR
XX 29-OCT-1999; 99US-0162498.

PR
XX 13-DEC-1999; 99US-0170453.

PR
XX 14-JAN-2000; 2000US-0176195.

PR
XX 14-FEB-2000; 2000US-0182296.

PR
XX 11-APR-2000; 2000US-0196460.

PR
XX 11-APR-2000; 2000US-0196527.

XX
PA (ARBO-) ARBOR VITA CORP.

XX
XX Lu PS;

PI
XX
XX WPI; 2001-061214/07.

DR
XX
XX Modulating a biological function of a hematopoietic cell for treating

PT an allergic response, or diseases mediated by immune system cells,
PT comprises introducing into the cell a PDZ-PL interaction enhancer or
PT inhibitor -
XX
PS Disclosure; Page 32; 143pp; English.
XX
XX The present invention relates to a method for modulating a biological
CC function of an endothelial cell or hematopoietic cell, comprises
CC introducing into a cell an antagonist that inhibits binding between a
CC PDZ domain protein and a PL domain protein to result in inhibition of
CC leukocyte activation. The present sequence is a PDZ domain. PDZ domains
CC of proteins are named after three prototypical proteins: PSD95,
CC prosophila large disc protein and zonula Occludin 1 protein. PDZ domain
CC proteins are involved in synapse formation by organising transmembrane
CC neurotransmitter receptors through intracellular interactions. The
CC inhibitors identified by the present invention can be used to treat a
CC disease mediated by hematopoietic cells, e.g. autoimmune disease,
CC inflammation, allergy (e.g. drug allergies), inflammatory bowel diseases,
CC ulcerative colitis, ileitis, psoriasis, respiratory allergic diseases
CC (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto
CC thyroiditis, osteoarthritis), atherosclerosis, cancers, infectious
CC diseases (e.g. viral infection), ischaemia, vasculitis and Crohn's
CC disease. The inhibitors can also be used to prevent transplantation
CC rejection of a solid organ transplant.

XX Sequence 97 AA:

Query Match 40.3%; Score 472; DB 22; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.6e-39;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 103 HSHPRVVELPTDEGLGFNVNMGKEQNSPIYISRIIPGVGVAERHGGKRGDQLLSVNGVS 162
Db 1 HSHPRVVELPTDEGLGFNVNMGKEQNSPIYISRIIPGVGVAERHGGKRGDQLLSVNGVS 60
QY 163 VEGEHHEKAVELLKAADSVKLVVRYTPKYLE 194
Db 61 VEGEHHEKAVELLKAADSVKLVVRYTPKYLE 92

GenCore version 5.1.1.6
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Perfect score: 1170
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 14893369 residues
Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0
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 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	807	69.0	207	15	Sequence 76, Appl
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22	807	69.0	207	15	US-10-232-231-76	Sequence 76, Appl
23	807	69.0	207	15	US-10-232-233-76	Sequence 76, Appl
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39	807	69.0	207	15	US-10-232-223-76	Sequence 76, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09909005
; Patent No. US20020082388A1
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
; FILE REFERENCE: PF-0599 US
; CURRENT APPLICATION NUMBER: US/09/909,005
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/370,102
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1974337
US-09-909-005-1

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Matches 233;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLKPSVTSAPTADMTLVVQPLTDRDVARAIELEKLOESGEVPHVKLSIKVQLQSE	60	
Db	1	MLKPSVTSAPTADMTLVVQPLTDRDVARAIELEKLOESGEVPHVKLSIKVQLQSE	60	
QY	61	FTATREYQYMHETITVNGCPFEFRARATAKATVAFAASEGSHSPRVVLEPKTDGLGF	120	
Db	61	FTATREYQYMHETITVNGCPFEFRARATAKATVAFAASEGSHSPRVVLEPKTDGLGF	120	
QY	121	NYMGKQNSPIYIIRIIPGVAERHGGKRGDQLSVNGSVSEGEHKEAYELLKAAND	180	

; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/095302
 ; PRIOR FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: 60/095318
 ; PRIOR FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: 60/095916
 ; PRIOR FILING DATE: 1998-08-10
 ; PRIOR APPLICATION NUMBER: 60/096146
 ; PRIOR FILING DATE: 1998-08-11
 ; PRIOR APPLICATION NUMBER: 60/096791
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: 60/097986
 ; PRIOR FILING DATE: 1998-08-26
 ; PRIOR APPLICATION NUMBER: 60/098544
 ; PRIOR FILING DATE: 1998-08-31
 ; PRIOR APPLICATION NUMBER: 60/099596
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 ; PRIOR APPLICATION NUMBER: 60/099598
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099803
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099811
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099812
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099816
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/100038
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: 60/100385
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100390
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100627
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100848
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/100919
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/101477
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101738
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101741
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101786
 ; PRIOR FILING DATE: 1998-09-25
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 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101922
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/106178
 ; PRIOR FILING DATE: 1998-10-28
 ; PRIOR APPLICATION NUMBER: 60/106248
 ; PRIOR FILING DATE: 1998-10-29
 ; PRIOR APPLICATION NUMBER: 60/106464
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: 60/106905
 ; PRIOR FILING DATE: 1998-11-03
 ; PRIOR APPLICATION NUMBER: 60/108787
 ; PRIOR FILING DATE: 1998-11-17
 ; PRIOR APPLICATION NUMBER: 60/108801
 ; PRIOR FILING DATE: 1998-11-17
 ; PRIOR APPLICATION NUMBER: 60/108849
 ; PRIOR FILING DATE: 1998-11-18
 ; PRIOR APPLICATION NUMBER: 60/112422
 ; PRIOR FILING DATE: 1998-12-15
 ; PRIOR APPLICATION NUMBER: 60/113296
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: 60/113605
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113621

; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/115558
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/115565
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/115733
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/119549
 ; PRIOR FILING DATE: 1999-02-10
 ; PRIOR APPLICATION NUMBER: 60/123618
 ; PRIOR FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: 60/125259
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 60/125775
 ; PRIOR FILING DATE: 1999-03-23
 ; PRIOR APPLICATION NUMBER: 60/126773
 ; PRIOR FILING DATE: 1999-03-29
 ; PRIOR APPLICATION NUMBER: 60/127887
 ; PRIOR FILING DATE: 1999-04-05
 ; PRIOR APPLICATION NUMBER: 60/130232
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/131022
 ; PRIOR FILING DATE: 1999-04-26
 ; PRIOR APPLICATION NUMBER: 60/131270
 ; PRIOR FILING DATE: 1999-04-27
 ; PRIOR APPLICATION NUMBER: 60/131291
 ; PRIOR FILING DATE: 1999-04-27
 ; PRIOR APPLICATION NUMBER: 60/131445
 ; PRIOR FILING DATE: 1999-04-28
 ; PRIOR APPLICATION NUMBER: 60/134287
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 60/140650
 ; PRIOR FILING DATE: 1999-06-22
 ; PRIOR APPLICATION NUMBER: 60/140723
 ; PRIOR FILING DATE: 1999-06-22
 ; PRIOR APPLICATION NUMBER: 60/141037
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/144758
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 60/145698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: 60/146222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: 60/146963
 ; PRIOR FILING DATE: 1999-08-03
 ; PRIOR APPLICATION NUMBER: 60/149320
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/149638
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/151733
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: 60/164418
 ; PRIOR FILING DATE: 1999-11-09
 ; PRIOR APPLICATION NUMBER: 60/166361
 ; PRIOR FILING DATE: 1999-11-16
 ; PRIOR APPLICATION NUMBER: 60/169445
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169835

Query Match 69.0%; Score 807; DB 15; Length 207;

Best Local Similarity 78.5%; Pred. No. 2.1e-70;

Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;

QY 14 MATLTVQPLTLDRDVARAIELEKQESGEVPHVKLSKVLQSEFCTAIREVQYMH 73

Db 1 MAAL--VEPLGLRDVSRVAVELLERLQSGELPPQKLQALQRLVQSFCSAIREVVEQLY 58

QY 74 ETTIVNGCPFRARATAKATVAFAASEGSHSPRVVELPKTDEGLGFNVMGKEQNSPIY 133

Db 59 DTLDITGSABIRAHATAKATVAFTASEGHAHPRVVELPKTDEGLGFNVMGKEQNSPIY 118

1 PRIOR APPLICATION NUMBER: 60/113296
2 PRIOR FILING DATE: 1998-12-22
3 PRIOR APPLICATION NUMBER: 60/113605
4 PRIOR FILING DATE: 1998-12-23
5 PRIOR APPLICATION NUMBER: 60/113621
6 PRIOR FILING DATE: 1998-12-23
7 PRIOR APPLICATION NUMBER: 60/115558
8 PRIOR FILING DATE: 1999-01-12
9 PRIOR APPLICATION NUMBER: 60/115565
10 PRIOR FILING DATE: 1999-01-12
11 PRIOR APPLICATION NUMBER: 60/115733
12 PRIOR FILING DATE: 1999-01-12
13 PRIOR APPLICATION NUMBER: 60/119549
14 PRIOR FILING DATE: 1999-02-10
15 PRIOR APPLICATION NUMBER: 60/123618
16 PRIOR FILING DATE: 1999-03-10
17 PRIOR APPLICATION NUMBER: 60/125259
18 PRIOR FILING DATE: 1999-03-19
19 PRIOR APPLICATION NUMBER: 60/125775
20 PRIOR FILING DATE: 1999-03-23
21 PRIOR APPLICATION NUMBER: 60/126773
22 PRIOR FILING DATE: 1999-03-29
23 PRIOR APPLICATION NUMBER: 60/127887
24 PRIOR FILING DATE: 1999-04-05
25 PRIOR APPLICATION NUMBER: 60/130232
26 PRIOR FILING DATE: 1999-04-21
27 PRIOR APPLICATION NUMBER: 60/131022
28 PRIOR FILING DATE: 1999-04-26
29 PRIOR APPLICATION NUMBER: 60/131270
30 PRIOR FILING DATE: 1999-04-27
31 PRIOR APPLICATION NUMBER: 60/131291
32 PRIOR FILING DATE: 1999-04-27
33 PRIOR APPLICATION NUMBER: 60/131445
34 PRIOR FILING DATE: 1999-04-28
35 PRIOR APPLICATION NUMBER: 60/134287
36 PRIOR FILING DATE: 1999-05-14
37 PRIOR APPLICATION NUMBER: 60/140650
38 PRIOR FILING DATE: 1999-06-22
39 PRIOR APPLICATION NUMBER: 60/140723
40 PRIOR FILING DATE: 1999-06-22
41 PRIOR APPLICATION NUMBER: 60/141037
42 PRIOR FILING DATE: 1999-06-23
43 PRIOR APPLICATION NUMBER: 60/144758
44 PRIOR FILING DATE: 1999-07-20
45 PRIOR APPLICATION NUMBER: 60/145698
46 PRIOR FILING DATE: 1999-07-26
47 PRIOR APPLICATION NUMBER: 60/146222
48 PRIOR FILING DATE: 1999-07-28
49 PRIOR APPLICATION NUMBER: 60/146963
50 PRIOR FILING DATE: 1999-08-03
51 PRIOR APPLICATION NUMBER: 60/149320
52 PRIOR FILING DATE: 1999-08-17
53 PRIOR APPLICATION NUMBER: 60/149638
54 PRIOR FILING DATE: 1999-08-17
55 PRIOR APPLICATION NUMBER: 60/151733
56 PRIOR FILING DATE: 1999-08-31
57 PRIOR APPLICATION NUMBER: 60/164418
58 PRIOR FILING DATE: 1999-11-09
59 PRIOR APPLICATION NUMBER: 60/166361
60 PRIOR FILING DATE: 1999-11-16
61 PRIOR APPLICATION NUMBER: 60/169445
62 PRIOR FILING DATE: 1999-12-07
63 PRIOR APPLICATION NUMBER: 60/169495
64 PRIOR FILING DATE: 1999-12-07
65 PRIOR APPLICATION NUMBER: 60/169835

Query Match 69.0%; Score 807; DB 15; Length 207;

Best Local Similarity 78.5%; Pred. No. 2.1e-70;

Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;

14 MATLTVVQPLTLDROVARAIELEKLOESGEVPHVKLSKLVQSEFCTAIREVYQYMH 73

1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKLOALQRLVQSRFCSAIREVYEQLY 58

14 MATLTVVQPLTLDROVARAIELEKLOESGEVPHVKLSKLVQSEFCTAIREVYQYMH 73

1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKLOALQRLVQSRFCSAIREVYEQLY 58

QY 74 ETITVNGCPEFRARATKATVAFAASEGHSHPRVVELPKTDGLGFNVWGKEQNSPIY 133
Db 59 DTLDTGSAEIRAHATAKATVAFAASEGHSHPRVVELPKTDGLGFNVWGKEQNSPIY 118
QY 134 ISRIIPGGVAERHGGGLKRGDQLLSVNGSVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193
Db 119 ISRVIPGGVADRHGGGLKRGDQLLSVNGSVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 178
QY 194 EEMEARFEKLRTARRRQQQQ 213
Db 179 EEMEARFEKMRSAARRRQQHQ 198

RESULT 5

US-10-149-819-19
; Sequence 19, Application US/10149819
; Publication No. US20030044913A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YOE, Henry
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: SHAH, Purvi
; APPLICANT: LAL, Preeti
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PF-0760 PCT
; CURRENT APPLICATION NUMBER: US/10/149,819
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
; PRIOR FILING DATE: 1999-12-10; 1999-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030044913A1 4062841CDI
US-10-149-819-19

Query Match 69.0%; Score 807; DB 15; Length 207;
Best Local Similarity 78.5%; Pred. No. 2.1e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;

QY 14 MATLTVVQPLTLDROVARAIELEKLOESGEVPHVKLSKLVQSEFCTAIREVYQYMH 73

Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKLOALQRLVQSRFCSAIREVYEQLY 58

QY 74 ETITVNGCPEFRARATKATVAFAASEGHSHPRVVELPKTDGLGFNVWGKEQNSPIY 133

Db 59 DTLDTGSAEIRAHATAKATVAFAASEGHSHPRVVELPKTDGLGFNVWGKEQNSPIY 118

QY 134 ISRIIPGGVAERHGGGLKRGDQLLSVNGSVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193

Db 119 ISRVIPGGVADRHGGGLKRGDQLLSVNGSVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 178

QY 194 EEMEARFEKLRTARRRQQQQ 213

Db 179 EEMEARFEKMRSAARRRQQHQ 198

RESULT 6

US-10-230-338-76

; Sequence 76, Application US/10230338

; Publication No. US20030044934A1

; GENERAL INFORMATION:


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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 76
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-76

Query Match      69.0%; Score 807; DB 15; Length 207;
Best Local Similarity 78.5%; Pred. No. 2.1e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;

QY 14 MATLVVQPLTDRVARAIELEKLEQSEVVPVHKLOSKVKVLOSEFCTAIREVYQYMH 73
Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKLQALQRLQSFCSAIREVYEQLY 58

QY 74 ETITVNGCPFRATATKATAFAASEGHSHSRVVELPKTDBGLGFNVMGKQKNSPIY 133
Db 59 DILDITGSAIRAHATAKATAVAFTASEGHAHPRVVELPKTDBGLGFNVMGKQKNSPIY 118

QY 134 ISRIIPGVAERGGKRGDQLLSVNGSVYEGHHEKAVELLKAAKDSVKLVVYTPKYL 193
Db 119 ISRVIPGVAERGGKRGDQLLSVNGSVYEGHHEKAVELLKAAQGSVKLVVYTPRVL 178

QY 194 EEMEARFEKLRTARRRQOOQ 213
Db 179 EEMEARFEKMSARRRQOHO 198

RESULT 11
US-10-227-873-76
; Sequence 76, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C72
; CURRENT APPLICATION NUMBER: US/10/227,873
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
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; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
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; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
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; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
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; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Best Match          69.0%; Score 807; DB 15; Length 207;
Query Local Similarity 78.5%; Pred. No. 2.le-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1

QY      14 MATLVTVQPLTLDSDVARATELLEKLOESGEVPHKLOSLKLVLOSEFCTAIREVYQYMH 73
Db      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MAAL--VEPLGLEKDXSRVAVELLERLQSRGELPQKLQALQKRVLOSRFCSAIREVTEQLY 58

QY      74 ETITVYNGPEPRARATKATYAAPAASEGSHSPRVVPELPKTDEGLGFNTVMGKEQNSPIY 133
Db      59 DTLDITGSAEIRAHATAKATYAAPTASEGHAHPRVVPELPKTDEGLGFNTVMGKEQNSPIY 118

QY      134 ISRIIPGVAVRHGHLKRGDOLLSVNGSVSYEGEHEKAVELLKAAKDSKLVVRYTPKVL 193
Db      119 ISRVIPGVAVRHGHLKRGDOLLSVNGSVSYEGEHEKAVELLKAAKDSKLVVRYTPKVL 193

QY      194 EMEARFEKLTARRRQQQ 213
Db      179 EMEARFEKMSARRRQQHQ 198

RESULT 12
US-10-227-883-76
; Sequence 76, Application US/10227883
; Publication No. US20030073817A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC78
; CURRENT APPLICATION NUMBER: US/10/227,883
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-27

Query Match
Best Local Similarity 14.8%; Score 173.5; DB 4; Length 724;
Matches 37; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

QY 106 PRVVELPKTDGLGNVNGKQNSPIYISRIIPGGVAERHGGKRGDQLLSVNGSVSEG 165
  || : : ||||| :||| : ||| : || : || : || : || : || : || : ||
Db 311 PRIVISRGSTGLGNTVGG-EDGEGIVISFILAGPWLDSGLRKGYQLLSVNGVDARN 369
  || : : ||||| :||| : ||| : || : || : || : || : || : || : ||
QY 166 EHHEKAVELLKAARDSVKLVVRYTPKYLEEMEAR 199
  || : : ||| : || : || : || : || : || : || : || : || : ||
Db 370 ASHEQADALKNAGQTVETIIAQYKPEEFSRFEAK 403
  || : : ||| : || : || : || : || : || : || : || : || : ||

RESULT 15
US-09-100-804-16
; Sequence 16, Application US/09100804
; Patent No. 6066472
; GENERAL INFORMATION:
; APPLICANT: GONZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,804
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/596,291
; FILING DATE: 09-AUG-1996
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: LO461/7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-100-804-16
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Query Match
Best Local Similarity 14.7%; Score 172.5; DB 3; Length 77;
Matches 35; Conservative 16; Mismatches 19; Indels 3; Gaps 1;

QY 117 GLGFNVMGKQEQ---NSPIYISRIIPGGVAERHGGKRGDQLLSVNGSVSEGEHEKAVE 173
  |||| :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 5 GLGFQIIGGERKMGRLDLGIFISSVAPGGPADFHGCLKPGDRLISVNSVSLGVSHHAAIE 64
  |||| :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 174 LKKAADSVKLVV 186
  || : : || : || : || : || : || : || : || : || : || : ||
Db 65 ILQNAPEDEVTLVI 77
  || : : || : || : || : || : || : || : || : || : || : ||
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Search completed: September 23, 2003, 15:15:45
Job time : 20 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2003, 15:13:08 ; Search time 17 Seconds
(without alignments)
579.908 Million cell updates/sec

Title: US-09-909-005-1
Perfect score: 1170
Sequence: 1 MLKPSVTSAPTADMATLTVLLIQOQQOQQOQQOQQOQQNHS 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1170	100.0	233	2	US-09-151-611-1
2	1170	100.0	233	3	US-09-370-102-1
3	643.5	55.0	297	2	US-09-151-611-3
4	643.5	55.0	297	3	US-09-370-102-3
5	196.5	16.8	724	4	US-09-562-737-21
6	190	16.2	1881	4	US-09-233-086-3
7	184	15.7	2465	2	US-08-596-291-3
8	184	15.7	2465	3	US-09-100-804-3
9	180.5	15.4	724	4	US-09-562-737-30
10	180.5	15.4	2466	3	US-09-080-855-12
11	180.5	15.4	2466	4	US-09-566-076-12
12	180.5	15.4	2466	5	PCT-US94-09943-2
13	174.5	14.9	2037	3	US-09-306-998-3
14	173.5	14.8	724	4	US-09-562-737-27
15	172.5	14.7	77	3	US-09-100-804-16
16	172.5	14.7	724	4	US-09-562-737-28
17	171	14.6	724	4	US-09-562-737-23
18	170.5	14.6	80	3	US-08-545-860D-54
19	170.5	14.6	80	5	PCT-US94-04496-54
20	169	14.4	2485	3	US-09-290-640-46
21	168.5	14.4	724	4	US-09-562-737-29
22	164.5	14.1	724	4	US-09-562-737-26
23	161.5	13.8	724	4	US-09-562-737-25
24	157.5	13.5	206	4	US-09-562-737-51
25	156.5	13.4	73	3	US-09-100-804-28
26	156.5	13.4	610	1	US-08-410-804-1
27	156.5	13.4	610	1	US-08-259-514-1

28 156.5 13.4 610 2 US-08-858-311-1 Sequence 1, Appli
29 155.5 13.3 73 3 US-09-100-804-25 Sequence 25, Appli
30 155 13.2 374 3 US-09-091-405-2 Sequence 2, Appli
31 155 13.2 631 4 US-09-147-119-7 Sequence 7, Appli
32 151.5 12.9 77 3 US-09-100-804-17 Sequence 17, Appli
33 149.5 12.8 724 4 US-09-562-737-24 Sequence 24, Appli
34 148.5 12.7 724 4 US-09-562-737-22 Sequence 22, Appli
35 148 12.6 632 4 US-09-996-243-219 Sequence 219, Appli
36 147.5 12.6 206 4 US-09-562-737-56 Sequence 56, Appli
37 147.5 12.6 505 1 US-08-123-161A-14 Sequence 14, Appli
38 147.5 12.6 505 1 US-08-483-278-14 Sequence 14, Appli
39 145.5 12.4 206 4 US-09-562-737-52 Sequence 52, Appli
40 145 12.4 358 4 US-09-740-027-4 Sequence 4, Appli
41 143.5 12.3 79 3 US-09-100-804-27 Sequence 27, Appli
42 143.5 12.3 86 3 US-08-545-860D-53 Sequence 53, Appli
43 143.5 12.3 86 5 PCT-US94-04496-53 Sequence 53, Appli
44 142.5 12.2 450 2 US-08-665-037-2 Sequence 2, Appli
45 142.5 12.2 450 2 US-08-666-067-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-151-611-1
; Sequence 1, Application US/09151611
; Patent No. 5958731
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
; FILE REFERENCE: PF-0599 US
; CURRENT APPLICATION NUMBER: US/09/151,611
; CURRENT FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1974337
US-09-151-611-1

Query Match 100.0%; Score 1170; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.5e-109;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLKPSVTSAPTADMATLTVVQPLTDRDVARAIELLEKLOESGVPVVKLSLKKVLOSE 60
Db 1 MLKPSVTSAPTADMATLTVVQPLTDRDVARAIELLEKLOESGVPVVKLSLKKVLOSE 60
Qy 61 FCTAIREYIQMHETITVNGCPEFRARATATVAFAASEGSHSPRVLPKTDGLGF 120
Db 61 FCTAIREYIQMHETITVNGCPEFRARATATVAFAASEGSHSPRVLPKTDGLGF 120
Qy 121 NVMGKKONSPYISRIIPGSAVRHGLKRGDOLLVNGSVSVEGEHEHKAVALLKAAD 180
Db 121 NVMGKKONSPYISRIIPGSAVRHGLKRGDOLLVNGSVSVEGEHEHKAVALLKAAD 180
Qy 181 SVKLWRYTPKVLMEAREFEKLTARRRQQQLLIQOQQOQQOQQOQQNHS 233
Db 181 SVKLWRYTPKVLMEAREFEKLTARRRQQQLLIQOQQOQQOQQOQQNHS 233

RESULT 2
US-09-370-102-1
; Sequence 1, Application US/09370102
; Patent No. 6265547
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice

RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
 DR EMBL: AE003750; AAF56389.1; -
 DR HSP; Q12959; 1PDR; 269; velli.
 DR FlyBase: FBgn039269; velli.
 DR InterPro: IPR004172; L27.
 DR InterPro: IPR004178; PDZ.
 DR Pfam: PF02828; L27; 1.
 DR Pfam: PF00595; PDZ; 1.
 DR SMART: SM00569; L27; 1.
 DR SMART: SM00228; PDZ; 1.
 DR PROSITE: PS0106; PDZ; 1.
 DR PROSITE: PS0106; PDZ; 1.
 SQ SEQUENCE 195 AA; 21493 MW; EF9DF5ED71A73FBC CRC64;
 Query Match 64.4%; Score 754; DB 5; Length 195;
 Best Local Similarity 77.9%; Pred. No. 8.3e-54;
 Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;
 QY 21 QPFLDRVARAIELEKLOESGEVPHKQSLKVKVQSEFCTAIREVYQYMHETITVNG 80
 DB 6 EPLTSLRSYDKRSIELLEKLOAGSDPTTKLAALQKVLNSDFMTSVREYVETVDIQG 65
 QY 81 CPEFRATATKATVAFAAASGHGHPRVLPKPTDEGLGFMVNGKQNSPIVISRIIPG 140
 DB 66 SHDVRSATATKATVAFAAASGHGHPRVLPKPTDEGLGFMVNGKQNSPIVISRIIPG 125
 QY 141 GVAERHGLKRGDQLLSVNGSVSGEHEHKAVELLKAOKSVKLVRYTKVLEEMEARF 200
 DB 126 GVAERHGLKRGDQLLSVNGSVSGEHEHKAVELLKAOKSVKLVRYTKVLEEMEARF 185
 QY 201 EKLRTARRQ 210
 DB 186 DKQRTARRQ 195
 RESULT 11
 Q8INT8
 ID Q8INT8 PRELIMINARY; PRT; 244 AA.
 AC Q8INT8
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE CG7662-PB.
 GN VELT.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Sutton G.G., Wortman J.R., Richards S., Ashburner M., Henderson S.N.,
 RA Ratton G.G., Whitehead I., Yandell M.D., Zhang Q., Chen L.X.,
 RA Wan K.H., Doyle C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Ratton G.G., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Adayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.F., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Beremand B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Hostin N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zhou X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celnik S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Ranzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C.A., Nunoo J.,
 RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Radecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003750; AAN14038.1; -
 SQ SEQUENCE 244 AA; 27467 MW; 0A464B355772A8A1 CRC64;
 Query Match 58.5%; Score 684.5; DB 5; Length 244;
 Best Local Similarity 59.8%; Pred. No. 5.2e-48;
 Matches 144; Conservative 20; Mismatches 24; Indels 53; Gaps 2;
 QY 21 QPFLDRVARAIELEKLOESGEVPHKQSLKVKVQSEFCTAIREVYQYMHETITVNG 80
 DB 6 EPLTSLRSYDKRSIELLEKLOAGSDPTTKLAALQKVLNSDFMTSVREYVETVDIQG 65
 QY 81 CPEFRATATKATVAFAAASGHGHPRVLPKPTDEGLGFMVNGKQNSPIVISRIIPG 116
 DB 66 SHDVRSATATKATVAFAAASGHGHPRVLPKPTDEGLGFMVNGKQNSPIVISRIIPG 125

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QY 117 -----GLGFNMVGKQNSPIYISRIIPGGVAERHGL 149
Db 126 KYRPRIVSIHLTKALSIENFCSEGLGFNMVGKQNSPIYISRIIPGGVADRHGGL 185
QY 150 KRGDQLLSVNGSVGEHEKAVELLKAADSKVLVRYTPKVLSEMEARFEKLTARR 209
Db 186 KRGDQLLSVNG--VVRENHEKAVELLKQAVGSKVLVRYTPKVLSEMEARFEKLTARR 243
QY 210 Q 210
Db 244 Q 244

RESULT 12
ID 017458 PRELIMINARY; PRT: 171 AA.
AC 017458;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 19.0 kDa protein (Fragment).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=99334538; PubMed=10406037;
RA Harrop R., Coulson P.S., Wilson R.A.;
RT "Characterization, cloning and immunogenicity of antigens released by
RL lung-stage larvae of Schistosoma mansoni.";
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AF030965; AAB86566.1; -.
DR HSP; P31016; IBEF.
DR InterPro; IPR004172; L27.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF02828; L27; 1.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 171 AA; 19000 MW; 69685F4108598063 CRC64;

Query Match 55.4%; Score 648.5; DB 5; Length 171;
Best Local Similarity 73.7%; Pred. No. 2.9e-45;
Matches 123; Conservative 26; Mismatches 17; Indels 1; Gaps 1;

QY 44 EPPVHKQLKQLQSECTAIREYIYQYMHETITVNGCPFRARAKATVAAPAAASGH 103
Db 4 EIQPSKLAALQRIQLQSDFCMDIREYEHYITVDINGSEEVKASAKATVAAPAAASGH 63
QY 104 SHPRVVELPKDGLGFNMVGKQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSV 163
Db 64 AHPRVIELPKNEGGLGFNMVGKQNSPIYISRXMPGGVADRHGGLKRGDQLLSVNGSV 123
QY 164 EGEHEKAVELLKAADSKVLVRYTPKVLSEMEARFEKLTARRQ 210
Db 124 ESEHERAVELLKLAQGTIVLVRYTPRILEMEARFDK-QKARRQ 169

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ID Q90245 PRELIMINARY; PRT: 316 AA.
AC Q90245;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Y54G11A.10 protein.
GN Y54G11A.10.

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OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wallis J.M.;
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=98519116;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AL034488; CAA22459.2; -.
DR HSP; Q12959; IPDR.
DR WormPep; Y54G11A.10; CE28370.
DR InterPro; IPR004172; L27.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF02828; L27; 1.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00569; L27; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
SQ SEQUENCE 315 AA; 35663 MW; E050959F2D29B8FF CRC64;

Query Match 55.3%; Score 647.5; DB 5; Length 316;
Best Local Similarity 67.9%; Pred. No. 7.6e-45;
Matches 129; Conservative 30; Mismatches 30; Indels 1; Gaps 1;

QY 25 LDRVVARAIELLEKLOESGEVPHKQLKQLQSECTAIREYIYQYMHETITVNGCPFE 84
Db 117 LERDYQRIELMEHVQKTGEVNNAKLASLQQLQSEFFGAVREYETVYESIDADTTPEI 176
QY 85 RARATAKATVAFAASEGSHPRVVELPKDGLGFNMVGKQNSPIYISRIIPGGVAE 144
Db 177 KAATAKATVAFAAAGSHAPRIVELPKDGLGFNMVGKQNSPIYISRIIPGGVAD 236
QY 145 RHGGLKRGDQLLSVNGSVGEHEKAVELLKAADSKVLVRYTPKVLSEMEARFEKLR 204
Db 237 RHGGLKRGDQLIAVNG-NVEAECHKAVDLLKSAVGSVKLVRYNPKLLDEMERFERQR 295
QY 205 TARRRQOQOL 214
Db 296 IRSTQOQSPTL 305

RESULT 14
ID P90976 PRELIMINARY; PRT: 297 AA.
AC P90976;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE LIN-7 (Fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96200771; PubMed=8612272;
RA Simke J.S., Kaech S.M., Harp S.A., Kim S.K.;
RT "LET-23 receptor localization by the cell junction protein LIN-7
RL during C. elegans vulval induction.";
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; U78092; AAB36684.1; -.
DR HSP; Q12959; IPDR.
DR InterPro; IPR004172; L27.
DR InterPro; IPR001478; PDZ.

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DR Pfam; PF02828; L27; 1.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00569; L27; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
FT NON_TER 297
SQ SEQUENCE 297 AA; 33580 MW; A8F15EDB90B0A90E CRC64;

Query Match      55.0%; Score 643.5; DB 5; Length 297;
Best Local Similarity 70.6%; Pred. No. 1.5e-44;
Matches 127; Conservative 29; Mismatches 23; Indels 1; Gaps 1;

QY 25 LRDVARAELELEKLGESGVPVHKLSKVLQSEFCTAIRVYQIMHETITVNGCPFF 84
Db 117 LERDVQRILELMEHVGTGEVNNAKLASLQVQLQSEFFGAVREYVETVESIDADTTPEI 176

QY 85 RARATAKATVAFAASEGSHSRPVVELPKTDEGLGNVNGGKEQNSPIYISRIIPGVAE 144
Db 177 KAAATAKATVAFAAAEGHAHPRIVELPKTDQGLGNVNGGKEQNSPIYISRIIPGVAD 236

QY 145 RHGGLKRGDQLLAVNG-NVEAECHAKAVDLLKSAVGSVKLVIRYMPKILDEMERFEROR 204
Db 237 RHGGLKRGDQLLAVNG-NVEAECHAKAVDLLKSAVGSVKLVIRYMPKILDEMERFEROR 295

RESULT 15
Q9BI79 PRELIMINARY; PRT; 967 AA.
AC Q9BI79;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MAGUK protein DLG-1 (SAP97-like protein DLG-1).
GN DLG-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RX MEDLINE=21385302; PubMed=11493666;
RA McMahon L., Legouis R., Vonesch J.L., Labouesse M.;
RT "Assembly of C. elegans apical junctions involves positioning and
RT compaction by LET-413 and protein aggregation by the MAGUK protein
RT DLG-1."
RL J. Cell Sci. 114:2265-2277(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=21385302; PubMed=11493666;
RA McMahon L., Legouis R., Vonesch J.L., Labouesse M.;
RT "Assembly of C. elegans apical junctions involves positioning and
RT compaction by LET-413 and protein aggregation by the MAGUK protein
RT DLG-1."
RL J. Cell Sci. 114:2265-2277(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Firestein B.L., Rongo C.;
RT "DLG-1 is a MAGUK similar to SAP97 and is required for adherens
RT junction formation."
RL Mol. Biol. Cell 0:0-0(2001).
CC -!- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AJ295228; CAC3153.1; -
DR EMBL; AF406786; RAL01376.1; -
DR HSP; Q12959; IPDR.
DR InterPro; IPR000619; Guanylate_kin.
DR InterPro; IPR004172; L27.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00595; PDZ; 3.
DR Pfam; PF00018; SH3; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00072; GUKC; 1.
DR SMART; SM00569; L27; 1.
DR SMART; SM00228; PDZ; 3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS00502; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS0106; PDZ; 3.
```

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DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 967 AA; 106991 MW; 44CDF119D6C6B368 CRC64;

Query Match      20.0%; Score 233.5; DB 5; Length 967;
Best Local Similarity 48.5%; Pred. No. 2e-10;
Matches 48; Conservative 18; Mismatches 32; Indels 1; Gaps 1;

QY 106 PRVVELPKTDEGLGNVNGGKEQNSPIYISRIIPGVAEHGLKRGDQLLSVNGSVSEG 165
Db 508 PRPVLVKGQNGLGNVGG-EDNEPIYISFVLPGGVADLSGNVKTGDLVLENGVYLRN 566

QY 166 EHHEKAVELLKAAKDSVKLVVRYTPKVLMEAEARFEKLR 204
Db 567 ATHKEAAEALRNAGNPVYLTLYRQEQYQIFESKIEKLR 605

Search completed: September 23, 2003, 15:14:58
Job time : 42 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:11:58 / Search time 37 Seconds
(without alignments)
1625.034 Million cell updates/sec

Title: US-09-909-005-1
Perfect score: 1170
Sequence: 1 MLKPSVTSAPTADMTLVV.....LLIQQQQQQQQQQQQQNHS 233

Scoring table: BLOSUM62
Gapop 10.0 / Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_protist.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rv.*
- 16: sp_bacteriophage.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1170	100.0	233	4	O14910	O14910 homo sapien
2	1077.5	92.1	219	11	O92250	O92250 rattus norv
3	1057	90.3	211	11	O81Z50	O81Z50 mus musculu
4	814	69.6	197	4	O9NUP9	O9NUP9 homo sapien
5	814	69.6	197	11	O88952	O88952 mus musculu
6	809	69.1	207	11	O88951	O88951 mus musculu
7	809	69.1	207	11	O92252	O92252 rattus norv
8	807	69.0	207	4	O9HAP6	O9HAP6 homo sapien
9	758	64.8	182	11	O92251	O92251 rattus norv
10	754	64.4	195	5	O9VEY7	O9VEY7 drosophila
11	684.5	58.5	244	5	O81MT8	O81MT8 drosophila
12	648.5	55.4	171	5	O17458	O17458 schistosoma
13	647.5	55.3	316	5	O9U245	O9U245 caenorhabdi
14	643.5	55.0	297	5	P90976	P90976 caenorhabdi
15	233.5	20.0	967	5	O9B179	O9B179 caenorhabdi
16	233.5	20.0	1064	5	O18165	O18165 caenorhabdi

17	219	18.7	852	11	O91XM9	O91XM9 mus musculu
18	208.5	17.8	960	5	O9VYZ4	O9VYZ4 drosophila
19	208.5	17.8	968	5	O9VYZ5	O9VYZ5 drosophila
20	199.5	17.1	403	11	O8BSV4	O8BSV4 mus musculu
21	199.5	17.1	455	11	O920R1	O920R1 mus musculu
22	199.5	17.1	455	11	O9ET11	O9ET11 mus musculu
23	199.5	17.1	463	11	O8BH60	O8BH60 mus musculu
24	198.5	17.0	454	4	O969U8	O969U8 homo sapien
25	198.5	17.0	462	4	O9HD26	O9HD26 homo sapien
26	196.5	16.8	721	11	O91WJ1	O91WJ1 mus musculu
27	192	16.4	893	11	O8CGN7	O8CGN7 mus musculu
28	191.5	16.4	2055	11	O921K3	O921K3 mus musculu
29	188.5	16.1	164	11	O8C0H8	O8C0H8 mus musculu
30	187.5	16.0	526	11	O08783	O08783 mus musculu
31	187.5	16.0	2055	11	O8VBY0	O8VBY0 mus musculu
32	187.5	16.0	2055	11	O8VBV5	O8VBV5 mus musculu
33	187.5	16.0	2055	11	O8VBX6	O8VBX6 mus musculu
34	186.5	15.9	2054	11	O55164	O55164 rattus norv
35	186	15.9	200	13	O9OX35	O9OX35 brachydanio
36	185	15.8	927	11	O62402	O62402 mus musculu
37	178.5	15.3	526	11	O8K4T6	O8K4T6 rattus norv
38	178.5	15.3	539	11	O8K4V4	O8K4V4 rattus norv
39	177	15.1	1012	5	O21075	O21075 caenorhabdi
40	176.5	15.1	2484	6	O28006	O28006 bos taurus
41	176	15.0	513	5	O19846	O19846 caenorhabdi
42	173	15.0	531	5	O9W486	O9W486 drosophila
43	174.5	14.9	453	4	O43798	O43798 homo sapien
44	174.5	14.9	517	4	O8N790	O8N790 homo sapien
45	174.5	14.9	582	4	O8WX31	O8WX31 homo sapien

ALIGNMENTS

RESULT 1					
O14910					
ID	O14910	PRELIMINARY;	PRT;	233 AA.	
AC	O14910:				
DT	01-JAN-1998	(TREMBLrel. 05, Created)			
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)			
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)			
DE	VELI 1	(TAX interaction protein 33) (Fragment).			
GN	MALS-1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_FaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Testis;				
RA	MEDLINE=98424246; PubMed=9753324;				
EX	Butz S., Okamoto M., Sudhof T.C.;				
FT	"A tripartite protein complex with the potential to couple synaptic				
RT	vesicle exocytosis to cell adhesion in brain."				
RL	Cell 94:773-782(1998).				
RN	[2]				
RP	SEQUENCE OF 32-233 FROM N.A.				
RA	Rousset R., Fabre S., Desbois C., Bantignies F., Jalinot P.;				
RL	Oncogene 15:0-0(1997).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99274724; PubMed=10341223;				
RA	Jo K., Derin R., Li M., Bredt D.S.;				
RT	"Characterization of MALS/Velis-1, -2, and -3: a family of mammalian				
RL	LIN-7 homologs enriched at brain synapses in association with the				
RT	postsynaptic density-95/NMDA receptor postsynaptic complex."				
RN	J. Neurosci. 19:4189-4199(1999).				
CC	-1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.				
EMBL	EMBL; AF087693; AAC78481.1; -				
DR	EMBL; AF028826; AAB84251.1; -				
DR	EMBL; AF173081; AAD48500.1; -				
DR	HSSP; Q12923; 3PDZ.				
DR	Genew; HGNC:17787; LIN7A.				

AF028826

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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:12:28 ; Search time 18 seconds

(without alignments)
1244.850 Million cell updates/sec

Title: US-09-909-005-1

Perfect score: 1170

Sequence: 1 MLKPSVTSAPTADMAITLV.....LLIQQQQQQQQQQQQQNHS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	662	56.6	317	2 T27179	hypothetical prote
2	233.5	20.0	1131	2 T15617	hypothetical prote
3	219	18.7	852	2 T10811	channel associated
4	217.5	18.6	870	2 G01974	discs-large tumor
5	208.5	17.8	960	1 A39651	synapse-associated
6	196.5	16.8	720	2 A45436	postsynaptic densi
7	196.5	16.8	724	2 JH0800	postsynaptic densi
8	196.5	16.8	767	2 T09599	homolog of Drosoph
9	192	16.4	904	2 T38757	synapse-associated
10	192	16.4	911	2 T36552	homolog of Drosoph
11	192	16.4	926	2 T38736	multiple PDZ domai
12	191.5	16.4	2055	2 T30259	multi PDZ domain p
13	186.5	15.9	2054	2 T46612	hypothetical prote
14	177	15.1	1012	2 T23160	hypothetical prote
15	176	15.0	431	2 T16191	protein-tyrosine-p
16	173.5	14.8	2450	2 S71625	protein-tyrosine-p
17	172.5	14.7	2466	2 T67629	protein-tyrosine-p
18	169	14.4	2294	2 T67630	tyrosine phosphata
19	167.5	14.3	117	2 T181209	tyrosine phosphata
20	167.5	14.3	126	2 T81210	probable guanilate
21	165	14.1	1171	2 T42372	brain-specific ang
22	165	14.1	1256	2 J80209	protein-tyrosine-p
23	165	14.1	2490	1 A54971	atypical protein k
24	161	13.8	1337	2 T13948	hypothetical prote
25	159	13.6	578	2 T13435	hypothetical prote
26	154.5	13.2	390	2 T28036	hypothetical prote
27	154.5	13.2	423	2 T21570	hypothetical prote
28	154.5	13.2	440	2 T21568	hypothetical prote
29	151	12.9	538	2 T59291	betal-syntrophin -

30	151	12.9	628	2 T09458	numb-binding prote
31	151	12.9	728	2 T09457	numb-binding prote
32	151	12.9	1112	2 T32733	AMPA glutamate rec
33	151	12.9	1277	2 T14152	synaptic scafoldi
34	150.5	12.9	87	2 S60315	PSD-95-related pro
35	147.5	12.6	488	2 T51379	svtrophin - Pacif
36	147.5	12.6	505	2 A53214	dystrophin-associa
37	146.5	12.5	503	2 T84771	svtrophin-1 - mou
38	145.5	12.4	505	2 S82894	alpha-syntrophin -
39	145.5	12.4	1893	2 A56158	eye development pr
40	144.5	12.4	450	2 G01158	tyrosine kinase ac
41	144.5	12.4	1281	2 T00346	hypothetical prote
42	142.5	12.2	358	2 T46532	protein co-factor
43	140.5	12.0	1095	2 T43275	neurabin - rat
44	138.5	11.8	2172	2 T20145	hypothetical prote
45	137.5	11.8	624	2 T19630	hypothetical prote

ALIGNMENTS

RESULT 1

T27179

Hypothetical protein Y54G11A.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27179

R:Wallis, J.

submitted to the EMBL Data Library, December 1998

A:Reference number: #20322

A:Accession: T27179

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-317 <WIL>

A:Cross-references: EMBL:AL034488; NID:el359895; PIDN:CAA22459.1; CESP:Y54G11A.10

A:Experimental source: clone Y54G11A

C:Genetics:

A:Gene: CESP:Y54G11A.10

A:Introns: 55/3; 108/3; 175/3; 228/2; 253/3

Query Match 56.6%; Score 662; DB 2; Length 317;

Best Local Similarity 68.4%; Pred. No. 2.5e-42;

Matches 130; Conservative 30; Mismatches 30; Indels 0; Gaps 0;

QY	25	LDROVARAIELEKLOESGEYVHKLSKLVLOSFECTAIREVYQYMHETITVNGCPEF	84
DB	117	LERDQVRILELMEHVQKTGEVNNAKLASLQOVLOSFEFFGAVREYETVYESIDATTPEI	176
QY	85	RARATAKATVAFAAASEGHSHPRVVELPKTDEGLGFNVMGKQNSPIYISRIIPGVAE	144
DB	177	KAATAKATVAFAAAGEGHAHPRIVELPKTDQGLGFNVMGKQNSPIYISRIIPGVAD	236
QY	145	RHGGLKRGDQLLSVNGSVSEGEHHEKAVELKAAKDSKLVVRYTPKYLEMEARFEKL	204
DB	237	RHGGLKRGDQLIAYNGVNVVEACHEKAVDLKSAVGSYKLVIRYMPKLLDEMERFERQ	296
QY	205	TARRRQQOOL 214	
DB	297	IRSTQQSPTL 306	

RESULT 2

T15617

Hypothetical protein C25F6.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15617

R:Bentley, D.

submitted to The EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid C25F6.

A:Reference number: T18377

A:Accession: T15617

A:Status: preliminary; translated from GB/EMBL/DBDJ

C:Accession: A45436
 R:Kistner, U.; Wenzel, B.M.; Veb, R.W.; Cases-Langhoff, C.; Garner, A.M.; Appeltauer, U.
 J. Biol. Chem. 268, 4580-4583, 1993
 A:Title: SAP90, a rat presynaptic protein related to the product of the Drosophila tumor
 A:Reference number: A45436; MUID:93186749; PMID:7680343
 A:Accession: A45436
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-720 <KIS>
 A:Experimental source: brain
 A:Note: sequence extracted from NCBI backbone (NCBIP:126555)
 C:Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase hom
 F:70-148/Domain: GLGF domain homology <GLG1>
 F:165-243/Domain: GLGF domain homology <GLG2>
 F:435-493/Domain: SH3 homology <SH3>
 F:531-708/Domain: guanylate kinase homology <GKI>
 Query Match 16.8%; Score 196.5; DB 2; Length 720;
 Best Local Similarity 41.4%; Pred. No. 5e-07;
 Matches 41; Conservative 19; Mismatches 38; Indels 1; Gaps 1;
 QY 106 PRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGVVAERHGGGLKRGDQLLSVNGSVYEG 165
 ||: : : |||||: || | : ||: : ||: : ||: : |||||: :
 Db 311 PRRIVHRGSGTGLGFNIYVG-EDGEGIFISFILAGPADLSGELKRGDQLLSVNGVDLNR 369
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 QY 166 EHHEKAVELLKAAKDSVKLVVRYTPKVLLEMEARPEKLK 204
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 Db 370 ASHEQAAIALKNAGQVTIIAQYKPEYSRFEAKIHLDR 408
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 RESULT 7
 JH0800
 postsynaptic density protein PSD-95 - rat
 N:Alternate names: brain specific PSD-95 protein; discs-large tumor suppressor protein h
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: JH0800; S26407
 R:Cho, K.O.; Hunt, C.A.; Kennedy, M.B.
 Neuron 9, 929-942, 1992
 A:Title: The rat brain postsynaptic density fraction contains a homolog of the drosophil
 A:Reference number: JH0800; MUID:93040233; PMID:1419001
 A:Accession: JH0800
 A:Molecule type: mRNA
 A:Residues: 1-724 <CHO>
 A:Cross-references: GB:M96853; NID:g206454; PTDN:AAA41971.1; PID:g206455
 A:Experimental source: brain
 C:Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase hom
 F:70-148/Domain: GLGF domain homology <GLG1>
 F:165-243/Domain: GLGF domain homology <GLG2>
 F:433-493/Domain: SH3 homology <SH3>
 F:535-712/Domain: guanylate kinase homology <GKI>
 Query Match 16.8%; Score 196.5; DB 2; Length 724;
 Best Local Similarity 41.4%; Pred. No. 5.1e-07;
 Matches 41; Conservative 19; Mismatches 38; Indels 1; Gaps 1;
 QY 106 PRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGVVAERHGGGLKRGDQLLSVNGSVYEG 165
 ||: : : |||||: || | : ||: : ||: : ||: : |||||: :
 Db 311 PRRIVHRGSGTGLGFNIYVG-EDGEGIFISFILAGPADLSGELKRGDQLLSVNGVDLNR 369
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 QY 166 EHHEKAVELLKAAKDSVKLVVRYTPKVLLEMEARPEKLK 204
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 Db 370 ASHEQAAIALKNAGQVTIIAQYKPEYSRFEAKIHLDR 408
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 RESULT 8
 T09599
 postsynaptic density protein 95 - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
 C:Accession: T09599
 R:Stathakis, D.G.; Hoover, K.H.; You, Z.; Bryant, P.J.
 submitted to the EMBL Data Library, July 1998

A:Reference number: Z16761
 A:Accession: T09599
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-767 <STA>
 A:Cross-references: EMBL:U83192; NID:g3318652; PID:g3318653
 A:Experimental source: mammary
 C:Genetics:
 A:Gene: PSD95
 C:Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase
 F:208-286/Domain: GLGF domain homology <GLG>
 F:478-536/Domain: SH3 homology <SH3>
 F:578-755/Domain: guanylate kinase homology <GKI>
 Query Match 16.8%; Score 196.5; DB 2; Length 767;
 Best Local Similarity 41.4%; Pred. No. 5.4e-07;
 Matches 41; Conservative 19; Mismatches 38; Indels 1; Gaps 1;
 QY 106 PRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGVVAERHGGGLKRGDQLLSVNGSVYEG 165
 ||: : : |||||: || | : ||: : ||: : ||: : |||||: :
 Db 354 PRRIVHRGSGTGLGFNIYVG-EDGEGIFISFILAGPADLSGELKRGDQLLSVNGVDLNR 412
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 QY 166 EHHEKAVELLKAAKDSVKLVVRYTPKVLLEMEARPEKLK 204
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 Db 413 ASHEQAAIALKNAGQVTIIAQYKPEYSRFEAKIHLDR 451
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 RESULT 9
 I38757
 homolog of Drosophila discs large protein, isoform 1 - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
 C:Accession: I38757
 R:Liue, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.
 Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994
 A:Title: Cloning and characterization of hdlg: the human homologue of the Drosophila
 A:Reference number: I38756; MUID:95024052; PMID:7937897
 A:Accession: I38757
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-904 <RES>
 A:Cross-references: EMBL:U13897; NID:g558437; PTDN:AAA50599.1; PID:g558438
 C:Genetics:
 A:Gene: GDB:DLG1
 A:Cross-references: GDB:393278; OMIM:601014
 A:Map position: 3q29-3q29
 C:Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase
 C:Keywords: alternative splicing; duplication
 F:229-307/Domain: GLGF domain homology <GLG1>
 F:324-402/Domain: GLGF domain homology <GLG2>
 F:588-646/Domain: SH3 homology <SH3>
 F:715-892/Domain: guanylate kinase homology <GKI>
 Query Match 16.4%; Score 192; DB 2; Length 904;
 Best Local Similarity 35.2%; Pred. No. 1.4e-06;
 Matches 44; Conservative 23; Mismatches 44; Indels 14; Gaps 2;
 QY 106 PRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGVVAERHGGGLKRGDQLLSVNGSVYEG 165
 ||: : : |||||: || | : ||: : ||: : ||: : |||||: :
 Db 464 PRKVVVHRGSGTGLGFNIYVG-EDGEGIFISFILAGPADLSGELKRGDRIISVNSVDLRA 522
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 QY 166 EHHEKAVELLKAAKDSVKLVVRYTPKVLLEMEARPEKLK-----TARRRQQ 212
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 Db 523 ASHEQAAALKNAGQAVTIIAQYKPEYSRFEAKIHLDRREQMNSSISSGSGSLRTSQKR 582
 ||: | ||: | : | : | : | : ||: ||: ||: ||
 QY 213 QLLIQ 217
 | : :
 Db 583 SLTVR 587
 RESULT 10
 I56552
 synapse-associated protein 97 - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jan-2000
C;Accession: I56552
R;Muller, B.M.; Kistner, U.; Veh, R.W.; Cases-Langhoff, C.; Becker, B.; Gundelfinger, E.
J. Neurosci. 15, 2354-2366, 1995
A;Title: Molecular characterization and spatial distribution of SAP97, a novel presynaptic protein from rat hippocampus
A;Reference number: I56552; MUID:95198112; PMID:7891172
A;Accession: I56552
A;Status: preliminary; translated from GE/EMBL/DDBB
A;Molecule type: mRNA
A;Residues: 1-911 <RES>
A;Cross-references: EMBL:U14950; NID:g642455; PIDN:AAA79976.1; PID:g642456
C;Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase homologous family
F;229-307/Domain: GLGF domain homology <GLG1>
F;323-401/Domain: GLGF domain homology <GLG2>
F;587-645/Domain: SH3 homology <SH3>
F;722-899/Domain: guanylate kinase homology <GKI>

Query Match 16.4%; Score 192; DB 2; Length 911;
Best Local Similarity 35.2%; Pred. No. 1.4e-06;
Matches 44; Conservative 23; Mismatches 44; Indels 14; Gaps 2;

QY 106 PRVVELPKTDEGLGFNMVGKQNPSPIYSRIIPGGVAERHGGIKRGDQLLSYNGSVSEG 165
||| : ||||||:|| | | | : | | : ||:::||| :
Db 463 PKVLVHRGSTGLGFNIIVGG-EDGEGIFISFIAGGPADLSGELRKGDRIISVNSVDLRA 521

QY 166 EHHEKAPELLAAKDVKLVRYTPPKVLEMEARFEKLRL-----TARRQQQ 212
||| : ||| : | | : | | : | | : ||| :
Db 522 ASHEQAAAAAKNQAGVATIAQAQRPEYSRFEAHIHLRETMMNSSVSSSGSGSLRTSQKR 581

QY 213 QLLIQ 217
| : : :
Db 582 SLVLR 586

RESULT 11
I38756
homolog of Drosophila discs large protein, isoform 2 - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C;Accession: I38756
R;Lue, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994
A;Title: Cloning and characterization of hdlg: the human homologue of the Drosophila discless homolog
A;Reference number: I38756; MUID:95024052; PMID:7937897
A;Accession: I38756
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-926 <RES>
A;Cross-references: EMBL:U13896; NID:g558435; PIDN:AAA50598.1; PID:g558436
C;Genetics:
A;Gene: GDB:DUG1
A;Cross-references: GDB:393278; OMIM:601014
A;Map position: 3q29-3q29
C;Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase homologous family
C;Keywords: alternative splicing; duplication
F;229-307/Domain: GLGF domain homology <GLG1>
F;324-402/Domain: GLGF domain homology <GLG2>
F;588-646/Domain: SH3 homology <SH3>
F;737-914/Domain: guanylate kinase homology <GKI>

Query Match 16.4%; Score 192; DB 2; Length 926;
Best Local Similarity 35.2%; Pred. No. 1.5e-06;
Matches 44; Conservative 23; Mismatches 44; Indels 14; Gaps 2;

QY 106 PRVVELPKTDEGLGFNMVGKQNPSPIYSRIIPGGVAERHGGIKRGDQLLSYNGSVSEG 165
||| : ||||||:|| | | | : | | : ||:::||| :
Db 464 PRKVLVHRGSTGLGFNIIVGG-EDGEGIFISFIAGGPADLSGELRKGDRIISVNSVDLRA 522

QY 166 EHHEKAPELLAAKDVKLVRYTPPKVLEMEARFEKLRL-----TARRQQQ 212
||| : ||| : | | : | | : | | : ||| :
Db 523 ASHEQAAAAAKNQAGVATIAQAQRPEYSRFEAHIHLRETMMNSSISSGSGSLRTSQKR 582

QY 57 LQSEFCTAIRVYOYMHETITVNGCPFRARATAKATVAFAASEGSHPRVVELPKTDE 116
Db 1938 TG-----HQEELANCLAF-----TGLTSTTFPDDLGPQSKTITLDRGPD 1979
QY 117 GLGNVNGG---KQNSPIYISRIIPGVAERHGLKRGDQLLSVNGSVSVEGEHEKAVE 173
Db 1980 GLGSIYGGYSGPHGLPIYVYKTFVAKGAAAEEDGRLKRGDQIIAVNGQSLGVTHEEAVA 2039
QY 174 LLKRAKDSVKLVV 186
Db 2040 ILKRTKGTVLNV 2052

RESULT 14

T23160
hypothetical protein K01A6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C:Accession: T23160
R:Cottage, A.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z19701
A:Accession: T23160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1012 <WIL>
A:Cross-references: EMBL:Z68750; PIDN:CAA92965.1; GSPDB:GNC00022; CESP:K01A6.1
A:Experimental source: clone K01A6
C:Genetics:
A:Gene: CESP:K01A6.1
A:Map position: 4
A:Introns: 107/1; 151/2; 183/2; 270/2; 316/3; 410/3; 628/3; 922/3; 971/3
C:Superfamily: WW repeat homology
F:131-168/Domain: WW repeat homology <WWR>

Query Match 15.1%; Score 177; DB 2; Length 1012;
Best Local Similarity 32.4%; Pred. No. 2.2e-05;
Matches 48; Conservative 30; Mismatches 50; Indels 20; Gaps 6;
QY 51 QSLKAKVLQSEFCTAIRVYOYMHETITVNGCPFRARATAKATVAAPAA-----SEGHS 104
Db 620 QNVENTLQKQ--PAVTSEWEGMSNAI-----PASMRPS--STTLGFATPNVILSQYNQ 670
QY 105 HPR---VVELPKTDEGLGNVNGGKEQNSPIYISRIIPGVAERHGLKRGDQLLSVNGV 161
Db 671 KPSDLITVSLIRKPVGFRLLGGVESKTPLSVGQIVIGAAAEEDGRLQEGDEIVEIDGH 730
QY 162 SVEGEHEKAVELLKAAKDS--VKLVVR 187
Db 731 NVEGASHEAVVLEAAAAONKHVKLIVR 758

RESULT 15

T16191
hypothetical protein F27D9.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16191
R:Bentley, D.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid F27D9.
A:Reference number: Z18473
A:Accession: T16191
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-431 <BEN>
A:Cross-references: EMBL:U49829; NID:g1203924; PID:g1203931; PIDN:AAA93388.1; CESP:F27D9.8
C:Genetics:
A:Gene: CESP:F27D9.8
A:Introns: 8/1; 52/3; 74/1; 96/1; 128/2; 149/3; 199/2; 255/3; 297/3; 319/3; 350/3; 390/3
Query Match 15.0%; Score 176; DB 2; Length 431;
Best Local Similarity 34.4%; Pred. No. 9.3e-06;

Matches 45; Conservative 26; Mismatches 46; Indels 14; Gaps 4;
QY 107 RVVELPKTDEGLGNVNGGKE--QNSPIYISRIIPGVAERHGLKRGDQLLSVNGSVSVE 164
Db 36 QWIVKKPDSGFGLSIKGGSENAQNMPIVISKIFKGLPADCEGELFGIDAIVEVNGISIE 95
QY 165 GEHEKAVELLKAAKDSVKLVVR---TP-----KVLE---EMEAREPEKLTARRRQQ 212
Db 96 QSHDEVVNMCLKSSGDQYTLGVRRHFTHTPFLKPAQSLOPDGTLDDQLDFGRSTRSHKAQS 155
QY 213 QLLIQQQQQQQ 223
Db 156 ESRLSDSKWQQ 166

Search completed: September 23, 2003, 15:15:21
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:11:13 : Search time 12 Seconds
(without alignments)
913.102 Million cell updates/sec

Title: US-09-909-005-1

Perfect score: 1170

Sequence: 1 MLKPSVTSAPADMAILTVV.....LLIQQQQQQQQQQQHMS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	219	18.7	852	1 DLG2_RAT	Q63622 rattus norv
2	217.5	18.6	870	1 DLG2_HUMAN	Q15700 homo sapien
3	208.5	17.8	960	1 DLG1_DROME	P31007 drosophila
4	203.5	17.4	817	1 DLG3_HUMAN	Q92796 homo sapien
5	203.5	17.4	849	1 DLG3_MOUSE	P70175 mus musculus
6	203.5	17.4	849	1 DLG3_RAT	Q62936 rattus norv
7	196.5	16.8	724	1 DLG4_MOUSE	Q62108 mus musculus
8	196.5	16.8	724	1 DLG4_RAT	P31016 rattus norv
9	196.5	16.8	767	1 DLG4_HUMAN	P78352 homo sapien
10	192	16.4	904	1 DLG1_HUMAN	Q12959 homo sapien
11	192	16.4	911	1 DLG1_RAT	Q62696 rattus norv
12	169	14.4	2485	1 PTND_HUMAN	Q12923 homo sapien
13	167	14.3	1356	1 PAD3_HUMAN	Q8tew0 homo sapien
14	161.5	13.8	1333	1 PAD3_MOUSE	Q99nh2 mus musculus
15	161	13.8	1337	1 PAD3_RAT	Q92340 rattus norv
16	160	13.7	540	1 SNB2_HUMAN	Q13425 homo sapien
17	158.5	13.5	520	1 SNB2_MOUSE	Q61235 mus musculus
18	158	13.5	537	1 SNB1_MOUSE	Q91188 mus musculus
19	158	13.5	637	1 MP4_HUMAN	Q961b8 homo sapien
20	157.5	13.5	206	1 SJ2B_RAT	Q9wvj4 rattus norv
21	157	13.4	539	1 SJ2B_HUMAN	Q9py99 homo sapien
22	155	13.2	631	1 IL16_HUMAN	Q14005 homo sapien
23	152.5	13.0	145	1 SJ2B_HUMAN	P57105 homo sapien
24	152.5	13.0	910	1 US1C_MOUSE	Q9se64 mus musculus
25	151	12.9	538	1 SNB1_HUMAN	Q13884 homo sapien
26	151	12.9	728	1 LNX1_MOUSE	Q70263 mus musculus
27	148	12.6	539	1 STG2_MOUSE	Q925e0 mus musculus
28	148	12.6	728	1 LNX1_HUMAN	Q8tbb1 homo sapien
29	147.5	12.6	505	1 SNAL_RABIT	Q28626 oryctolagus
30	146.5	12.5	503	1 SNAL_MOUSE	Q61234 mus musculus
31	145.5	12.4	505	1 SNAL_HUMAN	Q13424 homo sapien
32	145.5	12.4	552	1 US1C_HUMAN	Q9y6n9 homo sapien
33	144.5	12.4	1809	1 DLG5_HUMAN	Q8tdm6 homo sapien

34 143.5 12.3 742 1 NEB1_HUMAN Q9uij8 homo sapien
35 140.5 12.0 687 1 LNX2_MOUSE Q91xl2 mus musculus
36 140.5 12.0 1095 1 NEB1_RAT O35867 rattus norv
37 137.5 11.8 1026 1 PPL1_CAEEL P28191 caenorhabdi
38 137.5 11.8 1815 1 SHK3_RAT Q91lu4 rattus norv
39 137 11.7 1205 1 PA3L_HUMAN Q8tew8 homo sapien
40 136.5 11.7 690 1 LNX2_HUMAN Q8n448 homo sapien
41 134 11.5 517 1 STG1_HUMAN Q9psn8 homo sapien
42 133 11.4 517 1 STG1_MOUSE Q925el mus musculus
43 130.5 11.2 926 1 PTN4_HUMAN P29074 homo sapien
44 129 11.0 553 1 MPP6_MOUSE Q91lb0 mus musculus
45 126.5 10.8 5038 1 PCLO_MOUSE Q9gyx7 mus musculus

ALIGNMENTS

RESULT 1
DLG2_RAT STANDARD; PRT; 852 AA.
AC Q63622; P70548; Q62939;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Channel associated protein of synapse-110 (Chapsyn-110) (Synaptic density protein PSD-93) (Discs, large homolog 2).
GN DLG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96310881; PubMed=8755482;
RA Kim E., Cho K.O., Rothschild A., Sheng M.;
RT "Heteromultimerization and NMDA receptor-clustering activity of Chapsyn-110, a member of the PSD-95 family of proteins.";
RL Neuron 17:103-113(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96193770; PubMed=8625413;
RA Brenman J.E., Chao D.S., Gee S.H., McGee A.W., Craven S.E., Santillano D.R., Wu Z., Huang F., Xia H., Peters M.F., Froehner S.C., Bredt D.S.;
RT "Interaction of nitric oxide synthase with the postsynaptic density protein PSD-95 and alpha1-syntrophin mediated by PDZ domains.";
RL Cell 84:757-767(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX Irie M., Hata Y., Takai Y.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECEPTOR SUBUNITS AS WELL AS POTASSIUM CHANNELS.
CC -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; U49049; AAB53243.1; -
CC EMBL; U50717; AAC52643.1; -
CC EMBL; U53368; AAB48562.1; -
CC PIR; T10811; T10811.
CC HSP; Q12959; IPDR.
CC InterPro; IPR000619; Guanylate_kin.
CC InterPro; IPR001478; PDZ.

ID DLG1_DROME STANDARD; PRT; 960 AA.
AC P31007;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Discs large-1 tumor suppressor protein.
GN DLG1 OR L(1)DLG1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC TISSUE=Embryo;
RX MEDLINE=91330294; PubMed=1651169;
RA Woods D.F., Bryant P.J.;
RT "The discs-large tumor suppressor gene of Drosophila encodes a
RL guanylate kinase homolog localized at septate junctions.";
RL Cell 66:451-464(1991).
CC -!- FUNCTION: Plays a critical role at septate junctions in cellular
CC growth control during larval development. The presence of a
CC guanylate kinase domain suggests involvement in the presence of a
CC as well as signal transduction to control cellular proliferation.
CC Required for maintenance of cell polarity.
CC -!- SUBCELLULAR LOCATION: CYTOSKELETON-ASSOCIATED. LOCATED AT THE
CC CYTOPLASMIC FACE OF THE MEMBRANE IN THE CELLULAR BLASPOTERM AND
CC BECOMES ASSOCIATED WITH SEPTATE JUNCTIONS WHICH BEGIN TO FORM
CC BETWEEN EPITHELIAL CELLS AT THE TIME OF DORSAL CLOSURE. IN ADULT
CC FLIES, LOCATED AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF
CC EPITHELIAL CELLS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=1;
CC Comment-A number of isoforms are produced;
CC Name=1;
CC IsoId=P31007-1; Sequence=Displayed;
CC -!- TISSUE SPECIFICITY: In embryos, expression is seen in epithelial
CC cells and some nervous tissue. In larvae, expression is seen as a
CC belt around salivary glands and imaginal disks, also in
CC proventriculus and parts of the brain. Expressed in adult
CC reproductive tissues. Expressed both maternally and zygotically
CC -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically
CC throughout development.
CC -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@sib-sib.ch.
CC -----
DR EMBL; M73529; AAA28468.1; .
DR PIR; A39651; A39651.
DR HSP; P31016; 1BFE.
DR FlyBase; FBgn0001624; dlgl.
DR GO; GO:0045179; C:apical cortex; IDA.
DR GO; GO:0016327; C:apicolateral plasma membrane; IDA.
DR GO; GO:0005918; C:septate junction; NAS.
DR GO; GO:0045175; P:basal protein localization; IMP.
DR GO; GO:0007391; P:dorsal closure; NAS.
DR GO; GO:0045197; P:establishment and/or maintenance of epithel. . . ; NAS.
DR GO; GO:0016334; P:establishment and/or maintenance of polarit. . . ; IGI.
DR GO; GO:0016336; P:establishment and/or maintenance of polarit. . . ; IGI.
DR GO; GO:0007399; P:neurogenesis; IMP.
DR GO; GO:0007273; P:regulation of synapse; IMP.
DR InterPro; IPR000619; Guanylate_kin.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001452; SH3.

DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00595; PDZ; 3.
DR Pfam; PF00018; SH3; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00072; Gukc; 1.
DR SMART; SM00228; PDZ; 3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS00552; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS0106; PDZ; 3.
DR PROSITE; PS0002; SH3; 1.
KW Transducer; SH3 domain; Alternative splicing; Repeat.
FT DOMAIN 40 126 PDZ 1.
FT DOMAIN 154 244 PDZ 2.
FT DOMAIN 486 566 PDZ 3.
FT DOMAIN 600 670 SH3.
FT DOMAIN 768 960 GUANYLATE_KINASE.
SQ SEQUENCE 960 AA; 102468 MW; BF87A4262F1B6AD5 CRC64;
Query Match 17.8%; Score 208.5; DB 1; Length 960;
Best Local Similarity 39.3%; Pred. No. 9.2e-08;
Matches 46; Conservative 21; Mismatches 49; Indels 1; Gaps 1;
QY 88 ATAKATVAFAASEGSHPRVVELPKTDGLGFGNVMGKEQNSPIYSRIIPGGVAERHG 147
DB 466 AVPPCTPRAVSTEDITREPTTIQKPGQLGFGNIVGG-EDGGIYVSVILAGGRADLOS 524
QY 148 GUKRGDQLLSVNGSVSEGEHHEKAVELKAAKDSVKLVVYTPFKVLENEARFEKLR 204
DB 525 ELKRGDQLLSVNNVNLTHATEEAAQALKTSGGVVTLAQYRPEEYNFEARTQELK 581
RESULT 4
DLG3_HUMAN STANDARD; PRT; 817 AA.
AC Q92796; Q9ULI8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Presynaptic protein SAPI02 (Synapse-associated protein 102)
DE (Neuroendocrine-DLG) (NE-DLG) (Discs, large homolog 3).
GN DLG3 OR KIAA1232.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=97332623; PubMed=9188857;
RA Makino K., Kuwahara H., Masuko N., Nishiyama Y., Morisaki T.,
RA Sasaki J., Nakao M., Kuwano A., Nakata M., Ushio Y., Saya H.;
RT "Cloning and characterization of NE-dlg: a novel human homolog of the
RT Drosophila discs large (dlg) tumor suppressor protein interacts with
RT the APC protein.";
RL Oncogene 14:2425-2433(1997).
RN [2]
RP SEQUENCE OF 330-817 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K.-I., Kikuno R., Hirotsawa M., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
CC -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR
CC SUBUNIT NR2B (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.
CC -----

Db 370 ASHEQAALAKNAGQVTIIIAQYKPEYSRFEAKIHDLR 408

RESULT 8

DLG4_RAT

ID DLG4_RAT STANDARD; PRT; 724 AA.

AC P31016; P97631;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Presynaptic density protein 95 (PSD-95) (Presynaptic protein SAP90)

DE (Synapse-associated protein 90) (Discs, large homolog 4).

GN DLG4 OR PSD95.

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RX MEDLINE=93040233; PubMed=1419001;

RA Cho K.-O., Hunt C.A., Kennedy M.B.;

RT "The rat brain postsynaptic density fraction contains a homolog of

RT the Drosophila discs-large tumor suppressor protein.";

RL Neuron 9:929-942(1992).

RN [2]

SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RX MEDLINE=93186749; PubMed=7680343;

RA Kistner U., Wenzel B.M., Voh R.W., Cases-Langhoff C., Garner A.M.,

RA Apeltauer U., Voss B., Gundelfinger E.D., Garner C.C.;

RT "SAP90, a rat presynaptic protein related to the product of the

RT Drosophila tumor suppressor gene dlg-A.;

RL J. Biol. Chem. 268:4580-4583(1993).

RN [3]

SEQUENCE OF 566-625 FROM N.A.

RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;

RA Adams L.D., Werny I., Schwartz S.M.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

INTERACTION WITH DLGAP1 AND SHANK PROTEINS.

RC MEDLINE=99458653; PubMed=10527873;

RA Boeckers T.M., Winter C., Smalla K.-H., Kreutz M.R., Bockmann J.,

RA Seidenbecher C., Garner C.C., Gundelfinger E.D.;

RT "Proline-rich synapse-associated proteins Prosap1 and Prosap2 interact

RT with synaptic proteins of the SAPAP/GKAP family.;"

RL Biochem. Biophys. Res. Commun. 264:247-252(1999).

RN [5]

X-RAY CRYSTALLOGRAPHY (1.82 ANGSTROMS) OF 302-402.

RC MEDLINE=96270509; PubMed=8674113;

RA Doyle D.A., Lee A., Lewis J., Kim E., Sheng M., Mackinnon R.;

RT "Crystal structures of a complexed and peptide-free membrane protein-

RT binding domain: molecular basis of peptide recognition by PDZ.;"

RL Cell 85:1067-1076(1996).

CC -1- FUNCTION: Interacts with the cytoplasmic tail of NMDA receptor

CC subunits. May be involved in synaptogenesis.

CC -1- SUBUNIT: Interacts with DLGAP1/GKAP. Is part of a complex with

CC DLGAP1/GKAP, SHANK1 SHANK2 or SHANK3. Interacts through its third

CC PDZ domain with NLGN1, and probably with NLGN2 and NLGN3 (By

CC similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Concentrated at synaptic

CC junctions primarily on the presynaptic side. Also found in

CC postsynaptic density of neuronal cells.

CC -1- TISSUE SPECIFICITY: PRESYNAPTIC DENSITY FRACTION OF BRAIN.

CC -1- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.

CC -1- SIMILARITY: Contains 3 PDZ/DHR domains.

CC -1- SIMILARITY: Contains 1 SH3 domain.

CC -1- SIMILARITY: Contains 1 guanylate kinase-like domain.

CC

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CC or send an email to license@isb-sib.ch).

CC

DR EMBL; M96853; AAA41971.1; -

DR EMBL; X66474; CAA47103.1; -

DR EMBL; U77090; AAB38270.1; -

DR PIR; JH0800; JH0800.

DR PDB; 1BE9; 21-OCT-98.

DR PDB; 1BFE; 21-OCT-98.

DR PDB; 1JXM; 16-JAN-02.

DR PDB; 1KJW; 01-MAY-02.

DR PDB; 1QLC; 06-FEB-00.

DR InterPro; IPR000619; Guanylate_kin.

DR InterPro; IPR001478; PDZ.

DR InterPro; IPR001452; SH3.

DR Pfam; PF00625; Guanylate_kin; 1.

DR Pfam; PF00595; PDZ; 3.

DR ProDom; PD000066; SH3; 1.

DR SMART; SM00072; GUKC; 1.

DR SMART; SM00228; PDZ; 3.

DR SMART; SM00326; SH3; 1.

DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.

DR PROSITE; PS00502; GUANYLATE_KINASE_2; 1.

DR PROSITE; PS0106; PDZ; 3.

DR PROSITE; PS50002; SH3; 1.

DR SH3 domain; Repeat; 3D-structure.

FT DOMAIN 65 151 PDZ 1.

FT DOMAIN 160 246 PDZ 2.

FT DOMAIN 313 393 PDZ 3.

FT DOMAIN 428 498 SH3.

FT DOMAIN 534 724 GUANYLATE_KINASE.

FT CONFLICT 61 61 M -> L (IN REF. 2).

FT CONFLICT 78 78 S -> T (IN REF. 2).

FT CONFLICT 177 182 GVGNGH -> ALGTSI (IN REF. 2).

FT CONFLICT 200 200 A -> G (IN REF. 2).

FT CONFLICT 254 254 S -> T (IN REF. 2).

FT CONFLICT 540 555 LGPTKDRANDLLSEF -> SLDPPTKVTPTMIFSPS (IN REF. 2).

FT CONFLICT 623 625 GKX -> RDQ (IN REF. 3).

FT CONFLICT 724 724 AA; 80465 MW; 7922D4E90FAD85 CRC64;

Query Match 16.8%; Score 196.5; DB 1; Length 724;

Best Local Similarity 41.4%; Pred. No. 4.9e-07;

Matches 41; Conservative 19; Mismatches 38; Indels 1; Gaps 1;

QY 106 PRVVELPKTDEGLGFNMVGKEQNSPIYISRIIPGVVAERHGLKRGDQLSYNGVSEG 165

Db 311 PRVITHRGSTGLGFNIVGG-EDGEGITFSILAGGPADLSGELRGDQLSYNGVDLRN 369

QY 166 EHHEKAVELLKAAKDSVKLVVRYTPKVLMEARFEKLR 204

Db 370 ASHEQAALAKNAGQVTIIIAQYKPEYSRFEAKIHDLR 408

RESULT 9

DLG4_HUMAN

ID DLG4_HUMAN STANDARD; PRT; 767 AA.

AC P78352; Q92941; Q9UKK8;

DT 01-NOV-1997 (Rel. 35, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Presynaptic density protein 95 (PSD-95) (Discs, large homolog 4)

DE (Postsynaptic density-95).

GN DLG4 OR PSD95.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

SEQUENCE FROM N.A.

RP TISSUE=Mammary gland;

RX MEDLINE=97432822; PubMed=9286702;
 RT Stathakis D.G., Hoover K.B., You Z., Bryant P.J.;
 RA "Human postsynaptic density-95 (PSD95): location of the gene (DLG4)
 RL and possible function in nonneural as well as in neural tissues.";
 RN Genomics 44:71-82(1997).
 RN [2]
 RN
 RP REVISIONS.
 RP
 RC TISSUE=Mammary gland;
 RC Stathakis D.G., Hoover K.H., You Z., Bryant P.J.;
 RRL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RRL [3]
 RRL
 RP SEQUENCE FROM N.A.
 RP
 RX MEDLINE=20047407; PubMed=10582582;
 RA Stathakis D.G., Odar N., Sandgren O., Andreasson S., Bryant P.J.,
 RA Small K., Forsman-Semb K.;
 RL "Genomic organization of human DLG4, the gene encoding postsynaptic
 RT density 95.";
 RT J. Neurochem. 73:2250-2265(1999).
 RL [4]
 RN
 RN SEQUENCE OF 81-401 FROM N.A.
 RN
 RC TISSUE=Brain;
 RC Brennan J.E., Bredt D.S., Parkinson J.F., Manzana W.P., McClary J.A.;
 RRL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RRL [5]
 RRL
 RP INTERACTION WITH NLGN1; NLGN2 AND NLGN3.
 RP
 RX PubMed=9278515;
 RA Irie M., Hata Y., Takeuchi M., Ichchenko K., Toyoda A., Hirao K.,
 RA Takai Y., Rosahl T.W., Suedhof T.C.;
 RL "Binding of neuroligins to PSD-95";
 RT Science 277:1511-1515(1997).
 RL
 CC -!- FUNCTION: Interacts with the cytoplasmic tail of NMDA receptor
 CC subunits. May be involved in synaptogenesis.
 CC
 CC -!- SUBUNIT: Interacts with DLGAP1/GKAP (By similarity). Is part of a
 CC complex with DLGAP1/GKAP, SHANK1 SHANK2 or SHANK3 (By similarity).
 CC Binds to KIF13B. Interacts through its third PDZ domain with
 CC NLGN1, and probably with NLGN2 and NLGN3.
 CC
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Concentrated at synaptic
 CC junctions primarily on the presynaptic side. Also found in
 CC postsynaptic density of neuronal cells (By similarity).
 CC
 CC -!- TISSUE SPECIFICITY: BRAIN.
 CC
 CC -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
 CC
 CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.
 CC
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC
 CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.
 CC
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 DR EMBL; U83192; AAC52113.1; -;
 DR EMBL; AF156495; AAD56173.1; -;
 DR EMBL; U68138; BAB07736.1; -;
 DR PIR; T09599; T09599.
 DR PDB; 1KEF; 06-MAR-02.
 DR Genew; HGNC:2903; DLG4.
 DR MIM; 602887; -;
 DR GO; GO:0004384; F:membrane-associated guanylate kinase; TAS.
 DR GO; GO:0008022; F:protein C-terminus binding activity; TAS.
 DR GO; GO:0007612; P:learning; TAS.
 DR GO; GO:0007359; P:neurogenesis; TAS.
 DR GO; GO:0006461; P:protein complex assembly; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 DR InterPro; IPR000619; Guanylate_kin.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00625; Guanylate_kin; 1.
 DR Pfam; PF00595; PDZ; 3.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000066; SH3; 1.


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DR PROSITE; PS50002; SH3; 1.
KW SH3 domain; Repeat.
FT DOMAIN 224 310 PDZ 1.
FT DOMAIN 318 404 PDZ 2.
FT DOMAIN 465 545 PDZ 3.
FT DOMAIN 580 650 SH3.
FT DOMAIN 721 911 GUANYLATE KINASE.
FT DOMAIN 527 530 POLY-ALA.
SQ SEQUENCE 911 AA; 100570 MW; 18CEBD31DD0CAF8B CRC64;

Query Match 16.4%; Score 192; DB 1; Length 911;
Best Local Similarity 35.2%; Pred. No. 1.4e-06;
Matches 44; Conservative 23; Mismatches 44; Indels 14; Gaps 2;

QY 106 PRVVELPKTDEGGENVMGSGKEQNSPIYISRIIPGVAERHGLKRGDQLLSVNGSVSEG 165
DB 463 PRKVLHRSSTGLGFLNIVGG-EDGEGIFISFIAGGPADLSGELRGKDRISVNSVDLRA 521
QY 166 EHHEKAVELLKAARDSKVLVRYTPKYLEMEARFEKLR-----FARRRQQQ 212
DB 522 ASHEQAALKNAGQAVTIQAQYRPEYSRFEAKIHLDRETMMNSVYSGSGSLRTSQKR 581
QY 213 QLLIQ 217
DB 582 SLXVR 586

RESULT 12
PTND_HUMAN
ID PTND_HUMAN STANDARD; PRT; 2485 AA.
AC Q12923; Q15159; Q15263; Q15264; Q15265; Q16826;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase 1E) (PTP-El) (hPTP-El) (PTP-BAS)
DE phosphatase 1) (FAP-1).
DE PTPN13 OR PTPLE OR PTP11 OR PNP1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX TISSUE=Breast carcinoma;
RC SEQUENCE FROM N.A.
EX MEDLINE=94350988; PubMed=8071359;
RT "A novel protein-tyrosine phosphatase with homology to both the
RT cytoskeletal proteins of the band 4.1 family and junction-associated
RT guanylate kinases.";
RL J. Biol. Chem. 269:22320-22327(1994).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Leukemia;
RX MEDLINE=94116679; PubMed=8287977;
RA Maekawa K., Imagawa N., Nagamatsu M., Harada S.;
RT "Molecular cloning of a novel protein-tyrosine phosphatase containing
RT a membrane-binding domain and GLGF repeats.";
RL FEBS Lett. 337:200-206(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=95014139; PubMed=7929060;
RA Saras J., Claesson-Welsh L., Heldin C.-H., Gonen L.J.;
RT "Cloning and characterization of PTP11, a protein tyrosine phosphatase
RT with similarities to cytoskeletal-associated proteins.";
RL J. Biol. Chem. 269:24082-24089(1994).
RN [4]
RP SEQUENCE OF 1216-2490 FROM N.A.
RC TISSUE=Pancreas;
RA Wang H.Y.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.

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RN [5]
RP INTERACTION WITH TRIP6.
RX MEDLINE=99329089; PubMed=10400701;
RA Murthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.;
RT "ZRP-1, a zyxin-related protein, interacts with the second PDZ domain
RT of the cytosolic protein tyrosine phosphatase hPTP1E.";
RL J. Biol. Chem. 274:20679-20687(1999).
RN [6]
RP STRUCTURE BY NMR OF 1361-1456.
RX MEDLINE=20170882; PubMed=10704206;
RA Kozlov G., Gehring K., Ekiel I.;
RT "Solution structure of the PDZ2 domain from human phosphatase hPTP1E
RT and its interactions with C-terminal peptides from the Fas
RT receptor.";
RL Biochemistry 39:2572-2580(2000).
CC -1- FUNCTION: BINDS TO A NEGATIVE REGULATORY DOMAIN IN FAS THAT
CC INHIBITS FAS-INDUCED APOPTOSIS.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBUNIT: Interacts with TRIP6 and Fas receptor through its second
CC PDZ domain.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative Splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q12923-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q12923-2; Sequence=VSP_000496;
CC Name=3;
CC IsoId=Q12923-3; Sequence=VSP_000497;
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST TISSUES WITH THE EXCEPTION OF
CC THE LIVER AND SKELETAL MUSCLE. MOST ABUNDANT IN LUNG, KIDNEY AND
CC FETAL BRAIN.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
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CC EMBL; U12128; AAB60339.1; -
CC EMBL; D21209; BAA04750.1; -
CC EMBL; D21210; BAA04751.1; -
CC EMBL; D21211; BAA04752.1; -
CC EMBL; X80289; CAA56563.1; -
CC EMBL; X79676; CAA56124.1; -
CC PIR; A54971; A54971.
CC PIR; I67629; I67629.
CC PIR; I67630; I67630.
CC PDB; 3PDZ; 17-MAR-00.
CC PDB; ID5G; 24-JUL-02.
CC Genew; HGNC:9646; PTPN13.
CC MIM; 600267; -
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC InterPro; IPR000299; Band_4.1.
CC InterPro; IPR001478; PDZ.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00373; Band_41; 1.
CC Pfam; PF00595; PDZ; 5.
CC Pfam; PF0102; Y_phosphatase; 1.
CC PRINTS; PR00935; BAND41.
CC PRINTS; PR00700; PTPPHPTASE.
CC SMART; SM00295; B41; 1.
CC SMART; SM00228; PDZ; 5.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00660; FERM_1; FALSE_NEG.

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DR PROSITE; PS00661; FERM_2; FALSE_NEG.
DR PROSITE; PS50057; FERM_3; 1.
DR PROSITE; PS50106; PDZ_5.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Structural protein; Cytoskeleton; Hydrolase; Repeat; 3D-structure;
KW Alternative splicing; Coiled coil.
FT DOMAIN 56 59 POLY-LEU.
FT DOMAIN 572 872 FERM.
FT DOMAIN 2237 2485 PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN 379 399 COILED COIL (POTENTIAL).
FT DOMAIN 469 504 COILED COIL (POTENTIAL).
FT DOMAIN 1775 1804 COILED COIL (POTENTIAL).
FT DOMAIN 2057 2085 COILED COIL (POTENTIAL).
FT DOMAIN 1093 1178 PDZ 1.
FT DOMAIN 1368 1452 PDZ 2.
FT DOMAIN 1501 1588 PDZ 3.
FT DOMAIN 1788 1868 PDZ 4.
FT DOMAIN 1882 1965 PDZ 5.
FT DOMAIN 1742 1749 POLY-SER.
FT ACT_SITE 2408 2408 Missing (in isoform 2).
FT VARSPPLIC 884 1074 /FTID=VSP_000496.
FT VARSPPLIC 1056 1074 Missing (in isoform 3).
FT VARSPPLIC 1134 1135 /FTID=VSP_000497.
FT CONFLICT 1216 1229 LD -> FH (IN REF. 3).
FT CONFLICT 1238 1239 KDHWSRGTLRHIS -> DLRSRSHCHVLAHL (IN REF. 4).
FT CONFLICT 1238 1239 GL -> A (IN REF. 4).
FT CONFLICT 1357 1357 S -> P (IN REF. 4).
FT CONFLICT 1362 1363 KP -> RS (IN REF. 4).
FT CONFLICT 1383 1383 T -> TVLFDK (IN REF. 1).
FT CONFLICT 1538 1538 P -> A (IN REF. 3).
FT CONFLICT 1649 1649 R -> K (IN REF. 4).
FT CONFLICT 1698 1714 KSEDRTICTNFIYFQKI -> RVKKIPFVPCFILKKR (IN REF. 4).
FT CONFLICT 1797 1797 G -> A (IN REF. 3).
FT CONFLICT 1856 1797 AA -> G (IN REF. 4).
FT CONFLICT 2069 2069 A -> S (IN REF. 4).
FT CONFLICT 2206 2210 GLLDQ -> VARS (IN REF. 4).
FT STRAND 1366 1371
FT TURN 1373 1375
FT STRAND 1380 1384
FT TURN 1387 1389
FT STRAND 1395 1400
FT TURN 1402 1403
FT HELIX 1405 1409
FT TURN 1410 1410
FT TURN 1414 1415
FT STRAND 1417 1418
FT STRAND 1420 1421
FT TURN 1422 1423
FT STRAND 1424 1425
FT HELIX 1431 1439
FT STRAND 1445 1450
SQ SEQUENCE 2485 AA; 276903 MW; 8D1B31597C66962B CRC64;

Query Match 14.4%; Score 169; DB 1; Length 2485;
Best Local Similarity 28.4%; Pred. No. 0.00022;
Matches 40; Conservative 26; Mismatches 43; Indels 32; Gaps 2;

QY 78 VNGCPFRARATKATVAFAAEGSHSPR-----V 108
Db 1309 ISDVTYDSRGDSMDENYSSQDHTPKQESSSVNTSNKMFYFSSPPKPGDIFE 1368
QY 109 VELPKTDEGLGFNMVG---KEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSEG 165
Db 1369 VELAKNDNSLGISVGTGVNTSVRHGIIYKAVIPQGAESDGRHKGDRVIAVNGSVLEG 1428
QY 166 EHEKAVELLKAADSKLVW 186
Db 1429 ATHKQAVETLRNTGVVHLL 1449
```

```
RESULT 13
PAD3_HUMAN
ID PAD3_HUMAN STANDARD; PRT; 1356 AA.
AC Q8TEW0; Q8TEW1; Q8TEW2; Q8TEW3; Q96K28; Q96RM6; Q96RM7; Q9BY57;
AC Q9BY58; Q9HC48; Q9NWL4; Q9NVE6;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Partitioning-defective 3 homolog (PARD-3) (PAR-3) (Atypical PKC
5) isotype-specific interacting protein) (ASIP) (CTCL tumor antigen se2-
GN PARD3 OR PAR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND INTERACTION WITH PARD6B.
RC TISSUE=Kidney;
RX MEDLINE=20394296; PubMed=10934474;
RA Joberty G., Petersen C., Gao L., Macara I.G.;
RT "The cell-polarity protein Par6 links Par3 and atypical protein kinase
C to Cdc42.";
RL Nat. Cell Biol. 2:531-539(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 2; 3; 7; 8 AND 9).
RX PubMed=11642408;
RA Fang C.M., Xu Y.H.;
RT "Down-regulated expression of atypical PKC-binding domain deleted asip
isoforms in human hepatocellular carcinomas.";
RL Cell Res. 11:223-229(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6), INTERACTION WITH
PARD6B AND PRKCI; AND TISSUE SPECIFICITY.
RX PubMed=12234671;
RA Gao L., Macara I.G., Joberty G.;
RT "Multiple splice variants of Par3 and of a novel related gene, Par3L,
produce proteins with different binding properties.";
RL Gene 294:99-99(2002).
RN [4]
RP SEQUENCE OF 126-1356 FROM N.A. (ISOFORM 10).
RC TISSUE=Hepatoma, and Ovarian carcinoma;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takanashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 313-992 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21143360; PubMed=11149944;
RA Eichmüller S., Usener D., Dummer R., Stein A., Thiel D.,
RA Schadendorf D.;
RT "Serological detection of cutaneous T-cell lymphoma-associated
antigens.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:629-634(2001).
RN [6]
RP SEQUENCE OF 857-1356 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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